

SEQUENCE LISTING



(1) GENERAL INFORMATION:

- (i) APPLICANT: Ihle, James N.
Witthuhn, Bruce A.
Quelle, Frederick W.
Silvennoinen, Ollie
- (ii) TITLE OF INVENTION: Jak Kinases and Regulation of Cytokine Signal Transduction
- (iii) NUMBER OF SEQUENCES: 17
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Sterne, Kessler, Goldstein & Fox PLLC
 - (B) STREET: 1100 New York Avenue
 - (C) CITY: Washington
 - (D) STATE: D.C.
 - (E) COUNTRY: U.S.A.
 - (F) ZIP: 20005-3934
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: 09/397,967
 - (B) FILING DATE: 17-SEP-1999
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: 08/665,574
 - (B) FILING DATE: 18-JUN-1996
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: 08/282,012
 - (B) FILING DATE: 29-JUL-1994
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: 08/097,997
 - (B) FILING DATE: 29-JUL-1993
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Bugaisky, Lawrence B.
 - (B) REGISTRATION NUMBER: 35,086
 - (C) REFERENCE/DOCKET NUMBER: 0656.0370004/LBB/JAH
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: (202) 371-2600
 - (B) TELEFAX: (202) 371-2540

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 5 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Trp Ser Xaa Trp Ser
1 5

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Val Leu Pro Gln Asp Lys Glu Tyr Tyr Lys Val Lys Glu Pro Gly
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Ala Ile Glu Thr Asp Lys Glu Tyr Tyr Thr Val Lys Asp Asp Arg
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Ala Val Pro Glu Gly His Glu Tyr Tyr Arg Val Arg Glu Asp Gly
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Asp Ser Gln Arg Lys Leu Gln Phe Tyr Glu Asp Lys His Gln Leu Pro
1 5 10 15

Ala Pro Lys

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 19 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Thr Leu Ile Glu Lys Glu Arg Phe Tyr Glu Ser Arg Cys Arg Pro Val
1 5 10 15

Thr Pro Ser

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 19 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Ser Pro Ser Glu Lys Glu His Phe Tyr Gln Arg Gln His Arg Leu Pro
1 5 10 15

Glu Pro Ser

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 3629 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: CDS
 (B) LOCATION: 94..3480

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

CGGGGGAACA AGATGTGAAC TGTTTTCCCT CCCAGAAGA AGAGGCCCTT TTTTCCCTC 60
CCGCGAAGGC CAATGTTCTG AAAAAAGCTC TAG ATG GGA ATG GCC TGC CTT ACA 114
 Met Gly Met Ala Cys Leu Thr
 1 5
ATG ACA GAA ATG GAG GCA ACC TCC ACA TCT CCT GTA CAT CAG AAT GGT 162
Met Thr Glu Met Glu Ala Thr Ser Thr Ser Pro Val His Gln Asn Gly
 10 15 20
GAT ATT CCT GGA AGT GCT AAT TCT GTG AAG CAG ATA GAG CCA GTC CTT 210
Asp Ile Pro Gly Ser Ala Asn Ser Val Lys Gln Ile Glu Pro Val Leu
 25 30 35

CAA GTG TAT CTG TAC CAT TCT CTT GGG CAA GCT GAA GGA GAG TAT CTG Gln Val Tyr Leu Tyr His Ser Leu Gly Gln Ala Glu Gly Glu Tyr Leu 40 45 50 55	258
AAG TTT CCA AGT GGA GAG TAT GTT GCA GAA GAA ATT TGT GTG GCT GCT Lys Phe Pro Ser Gly Glu Tyr Val Ala Glu Glu Ile Cys Val Ala Ala 60 65 70	306
TCT AAA GCT TGT GGT ATT ACG CCT GTG TAT CAT AAT ATG TTT GCG TTA Ser Lys Ala Cys Gly Ile Thr Pro Val Tyr His Asn Met Phe Ala Leu 75 80 85	354
ATG AGT GAA ACC GAA AGG ATC TGG TAC CCA CCC AAT CAT GTC TTC CAC Met Ser Glu Thr Glu Arg Ile Trp Tyr Pro Pro Asn His Val Phe His 90 95 100	402
ATA GAC GAG TCA ACC AGG CAT GAC ATA CTC TAC AGG ATA AGG TTC TAC Ile Asp Glu Ser Thr Arg His Asp Ile Leu Tyr Arg Ile Arg Phe Tyr 105 110 115	450
TTC CCT CAT TGG TAC TGT AGT GGC AGC AGC AGA ACC TAC AGA TAC GGA Phe Pro His Trp Tyr Cys Ser Gly Ser Ser Arg Thr Tyr Arg Tyr Gly 120 125 130 135	498
GTG TCC CGT GGG GCT GAA GCT CCT CTG CTT GAT GAC TTT GTC ATG TCT Val Ser Arg Gly Ala Glu Ala Pro Leu Leu Asp Asp Phe Val Met Ser 140 145 150	546
TAC CTT TTT GCT CAG TGG CGG CAT GAT TTT GTT CAC GGA TGG ATA AAA Tyr Leu Phe Ala Gln Trp Arg His Asp Phe Val His Gly Trp Ile Lys 155 160 165	594
GTA CCT GTG ACT CAT GAA ACT CAG GAA GAG TGT CTT GGG ATG GCG GTG Val Pro Val Thr His Glu Thr Gln Glu Glu Cys Leu Gly Met Ala Val 170 175 180	642
TTA GAC ATG ATG AGA ATA GCT AAG GAG AAA GAC CAG ACT CCA CTG GCT Leu Asp Met Met Arg Ile Ala Lys Glu Lys Asp Gln Thr Pro Leu Ala 185 190 195	690
GTC TAT AAC TCT GTC AGC TAC AAG ACA TTC TTA CCA AAG TGC GTT CGA Val Tyr Asn Ser Val Ser Tyr Lys Thr Phe Leu Pro Lys Cys Val Arg 200 205 210 215	738
GCG AAG ATC CAA GAC TAT CAC ATT TTA ACC CGG AAG CGA ATC AGG TAC Ala Lys Ile Gln Asp Tyr His Ile Leu Thr Arg Lys Arg Ile Arg Tyr 220 225 230	786
AGA TTT CGC AGA TTC ATT CAG CAA TTC AGT CAA TGT AAA GCC ACT GCC Arg Phe Arg Arg Phe Ile Gln Gln Phe Ser Gln Cys Lys Ala Thr Ala 235 240 245	834
AGG AAC CTA AAA CTT AAG TAT CTT ATA AAC CTG GAA ACC CTG CAG TCT Arg Asn Leu Lys Leu Lys Tyr Leu Ile Asn Leu Glu Thr Leu Gln Ser 250 255 260	882
GCC TTC TAC ACA GAA CAG TTT GAA GTA AAA GAA TCT GCA AGA GGT CCT Ala Phe Tyr Thr Glu Gln Phe Glu Val Lys Glu Ser Ala Arg Gly Pro 265 270 275	930
TCA GGT GAG GAG ATT TTT GCA ACC ATT ATA ATA ACT GGA AAC GGT GGA Ser Gly Glu Glu Ile Phe Ala Thr Ile Ile Ile Thr Gly Asn Gly Gly	978

280	285	290	295	
ATT CAG TGG TCA AGA GGG AAA CAT AAG GAA AGT GAG ACA CTG ACA GAA Ile Gln Trp Ser Arg Gly Lys His Lys Glu Ser Glu Thr Leu Thr Glu 300 305 310				1026
CAG GAC GTA CAG TTA TAT TGT GAT TTC CCT GAT ATT ATT GAT GTC AGT Gln Asp Val Gln Leu Tyr Cys Asp Phe Pro Asp Ile Ile Asp Val Ser 315 320 325				1074
ATT AAG CAA GCA AAC CAG GAA TGC TCA AAT GAA AGT AGA ATT GTA ACT Ile Lys Gln Ala Asn Gln Glu Cys Ser Asn Glu Ser Arg Ile Val Thr 330 335 340				1122
GTC CAT AAA CAA GAT GGT AAA GTT TTG GAG ATA GAA CTT AGC TCA TTA Val His Lys Gln Asp Gly Lys Val Leu Glu Ile Glu Leu Ser Ser Leu 345 350 355				1170
AAA GAA GCC TTG TCA TTC GTG TCA TTA ATT GAC GGG TAT TAC AGA CTA Lys Glu Ala Leu Ser Phe Val Ser Leu Ile Asp Gly Tyr Tyr Arg Leu 360 365 370 375				1218
ACT GCG GAT GCG CAC CAT TAC CTC TGC AAA GAG GTG GCT CCC CCA GCT Thr Ala Asp Ala His His Tyr Leu Cys Lys Glu Val Ala Pro Pro Ala 380 385 390				1266
GTG CTC GAG AAC ATA CAC AGC AAC TGC CAC GGC CCA ATA TCA ATG GAT Val Leu Glu Asn Ile His Ser Asn Cys His Gly Pro Ile Ser Met Asp 395 400 405				1314
TTT GCC ATT AGC AAA CTA AAG AAG GCG GGT AAC CAG ACT GGA CTA TAT Phe Ala Ile Ser Lys Leu Lys Lys Ala Gly Asn Gln Thr Gly Leu Tyr 410 415 420				1362
GTG CTA CGA TGC AGC CCT AAG GAC TTC AAC AAA TAC TTT CTG ACC TTT Val Leu Arg Cys Ser Pro Lys Asp Phe Asn Lys Tyr Phe Leu Thr Phe 425 430 435				1410
GCT GTT GAG CGA GAA AAT GTC ATT GAA TAT AAA CAC TGT TTG ATT ACG Ala Val Glu Arg Glu Asn Val Ile Glu Tyr Lys His Cys Leu Ile Thr 440 445 450 455				1458
AAG AAT GAG AAT GGA GAA TAC AAC CTC AGC GGG ACT AAG AGG AAC TTC Lys Asn Glu Asn Gly Glu Tyr Asn Leu Ser Gly Thr Lys Arg Asn Phe 460 465 470				1506
AGT AAC CTT AAG GAC CTT TTG AAT TGC TAC CAG ATG GAA ACT GTG CGC Ser Asn Leu Lys Asp Leu Leu Asn Cys Tyr Gln Met Glu Thr Val Arg 475 480 485				1554
TCA GAC AGT ATC ATC TTC CAG TTT ACC AAA TGC TGC CCC CCA AAG CCA Ser Asp Ser Ile Ile Phe Gln Phe Thr Lys Cys Cys Pro Pro Lys Pro 490 495 500				1602
AAA GAT AAA TCA AAC CTT CTC GTC TTC AGA ACA AAT GGT ATT TCT GAT Lys Asp Lys Ser Asn Leu Leu Val Phe Arg Thr Asn Gly Ile Ser Asp 505 510 515				1650
GTT CAG ATC TCA CCA ACA TTA CAG AGG CAT AAT AAT GTG AAT CAA ATG Val Gln Ile Ser Pro Thr Leu Gln Arg His Asn Asn Val Asn Gln Met 520 525 530 535				1698

GTG TTT CAC AAA ATC AGG AAT GAA GAT TTA ATA TTT AAT GAA AGT CTT Val Phe His Lys Ile Arg Asn Glu Asp Leu Ile Phe Asn Glu Ser Leu 540 545 550	1746
GGC CAA GGT ACT TTT ACA AAA ATT TTT AAA GGT GTA AGA AGA GAA GTT Gly Gln Gly Thr Phe Thr Lys Ile Phe Lys Gly Val Arg Arg Glu Val 555 560 565	1794
GGA GAT TAT GGT CAA CTG CAC AAA ACG GAA GTT CTT TTG AAA GTC CTA Gly Asp Tyr Gly Gln Leu His Lys Thr Glu Val Leu Lys Val Leu 570 575 580	1842
GAT AAA GCA CAT AGG AAC TAT TCA GAG TCT TTC TTC GAA GCA GCA AGC Asp Lys Ala His Arg Asn Tyr Ser Glu Ser Phe Phe Glu Ala Ala Ser 585 590 595	1890
ATG ATG AGT CAG CTT TCT CAC AAG CAT TTG GTT TTG AAT TAT GGT GTC Met Met Ser Gln Leu Ser His Lys His Leu Val Leu Asn Tyr Gly Val 600 605 610 615	1938
TGT GTC TGT GGA GAG GAG AAC ATT CTG GTT CAA GAA TTT GTA AAA TTT Cys Val Cys Gly Glu Glu Asn Ile Leu Val Gln Glu Phe Val Lys Phe 620 625 630	1986
GGA TCA CTG GAT ACA TAC CTG AAG AAG AAC AAA AAT TCC ATA AAT ATA Gly Ser Leu Asp Thr Tyr Leu Lys Lys Asn Lys Asn Ser Ile Asn Ile 635 640 645	2034
TTA TGG AAA CTT GGA GTG GCT AAG CAG TTG GCA TGG GCC ATG CAT TTT Leu Trp Lys Leu Gly Val Ala Lys Gln Leu Ala Trp Ala Met His Phe 650 655 660	2082
CTA GAA GAA AAA TCC CTT ATT CAT GGG AAT GTG TGT GCT AAA AAT ATC Leu Glu Glu Lys Ser Leu Ile His Gly Asn Val Cys Ala Lys Asn Ile 665 670 675	2130
CTG CTT ATC AGA GAA GAA GAC AGG AGA ACG GGG AAC CCA CCT TTC ATC Leu Leu Ile Arg Glu Glu Asp Arg Arg Thr Gly Asn Pro Pro Phe Ile 680 685 690 695	2178
AAA CTT AGT GAT CCT GGC ATT AGC ATT ACA GTT CTA CCG AAG GAC ATT Lys Leu Ser Asp Pro Gly Ile Ser Ile Thr Val Leu Pro Lys Asp Ile 700 705 710	2226
CTT CAG GAG AGA ATA CCA TGG GTA CCT CCT GAA TGC ATT GAG AAT CCT Leu Gln Glu Arg Ile Pro Trp Val Pro Pro Glu Cys Ile Glu Asn Pro 715 720 725	2274
AAA AAT CTC AAT CTG GCA ACA GAC AAG TGG AGC TTC GGG ACC ACT CTG Lys Asn Leu Asn Leu Ala Thr Asp Lys Trp Ser Phe Gly Thr Thr Leu 730 735 740	2322
TGG GAG ATC TGC AGT GGA GGA GAT AAG CCC CTG AGT GCT CTG GAT TCT Trp Glu Ile Cys Ser Gly Gly Asp Lys Pro Leu Ser Ala Leu Asp Ser 745 750 755	2370
CAA AGA AAG CTG CAG TTC TAT GAA GAT AAG CAT CAG CTT CCT GCA CCC Gln Arg Lys Leu Gln Phe Tyr Glu Asp Lys His Gln Leu Pro Ala Pro 760 765 770 775	2418
AAG TGG ACA GAG TTA GCA AAC CTT ATA AAT AAT TGC ATG GAC TAT GAG Lys Trp Thr Glu Leu Ala Asn Leu Ile Asn Asn Cys Met Asp Tyr Glu	2466

				780				785				790							
CCA	GAT	TTC	AGG	CCT	GCT	TTC	AGA	GCT	GTC	ATC	CGT	GAT	CTT	AAC	AGC	2514			
Pro	Asp	Phe	Arg	Pro	Ala	Phe	Arg	Ala	Val	Ile	Arg	Asp	Leu	Asn	Ser				
795								800				805							
CTG	TTT	ACT	CCA	GAT	TAT	GAA	CTA	CTA	ACA	GAA	AAT	GAC	ATG	CTA	CCA	2562			
Leu	Phe	Thr	Pro	Asp	Tyr	Glu	Leu	Leu	Thr	Glu	Asn	Asp	Met	Leu	Pro				
810								815				820							
AAC	ATG	AGA	ATA	GGT	GCC	CTA	GGG	TTT	TCT	GGT	GCT	TTT	GAA	GAC	AGG	2610			
Asn	Met	Arg	Ile	Gly	Ala	Leu	Gly	Phe	Ser	Gly	Ala	Phe	Glu	Asp	Arg				
825								830				835							
GAC	CCT	ACA	CAG	TTT	GAA	GAG	AGA	CAC	TTG	AAG	TTT	CTA	CAG	CAG	CTT	2658			
Asp	Pro	Thr	Gln	Phe	Glu	Glu	Arg	His	Leu	Lys	Phe	Leu	Gln	Gln	Leu				
840				845				850				855							
GGC	AAA	GGT	AAC	TTC	GGG	AGT	GTG	GAG	ATG	TGC	CGC	TAT	GAC	CCG	CTG	2706			
Gly	Lys	Gly	Asn	Phe	Gly	Ser	Val	Glu	Met	Cys	Arg	Tyr	Asp	Pro	Leu				
				860				865				870							
CAG	GAC	AAC	ACT	GGC	GAG	GTG	GTC	GCT	GTG	AAG	AAA	CTC	CAG	CAC	AGC	2754			
Gln	Asp	Asn	Thr	Gly	Glu	Val	Val	Ala	Val	Lys	Lys	Leu	Gln	His	Ser				
875								880				885							
ACT	GAA	GAG	CAC	CTC	CGA	GAC	TTT	GAG	AGG	GAG	ATC	GAG	ATC	CTG	AAA	2802			
Thr	Glu	Glu	His	Leu	Arg	Asp	Phe	Glu	Arg	Glu	Ile	Glu	Ile	Leu	Lys				
890								895				900							
TCC	TTG	CAG	CAT	GAC	AAC	ATC	GTC	AAG	TAC	AAG	GGA	GTG	TGC	TAC	AGT	2850			
Ser	Leu	Gln	His	Asp	Asn	Ile	Val	Lys	Tyr	Lys	Gly	Val	Cys	Tyr	Ser				
905				910				915											
GCG	GGT	CGG	CGC	AAC	CTA	AGA	TTA	ATT	ATG	GAA	TAT	TTA	CCA	TAT	GGA	2898			
Ala	Gly	Arg	Arg	Asn	Leu	Arg	Leu	Ile	Met	Glu	Tyr	Leu	Pro	Tyr	Gly				
920				925				930				935							
AGT	TTA	CGA	GAC	TAT	CTC	CAA	AAA	CAT	AAA	GAA	CGG	ATA	GAT	CAC	AAA	2946			
Ser	Leu	Arg	Asp	Tyr	Leu	Gln	Lys	His	Lys	Glu	Arg	Ile	Asp	His	Lys				
				940				945				950							
AAA	CTT	CTT	CAA	TAC	ACA	TCT	CAG	ATA	TGC	AAG	GGC	ATG	GAA	TAT	CTT	2994			
Lys	Leu	Leu	Gln	Tyr	Thr	Ser	Gln	Ile	Cys	Lys	Gly	Met	Glu	Tyr	Leu				
955								960				965							
GGT	ACA	AAA	AGG	TAT	ATC	CAC	AGG	GAC	CTG	GCA	ACA	AGG	AAC	ATA	TTG	3042			
Gly	Thr	Lys	Arg	Tyr	Ile	His	Arg	Asp	Leu	Ala	Thr	Arg	Asn	Ile	Leu				
970								975				980							
GTG	GAA	AAT	GAG	AAC	AGG	GTT	AAA	ATA	GGA	GAC	TTC	GGA	TTA	ACC	AAA	3090			
Val	Glu	Asn	Glu	Asn	Arg	Val	Lys	Ile	Gly	Asp	Phe	Gly	Leu	Thr	Lys				
985				990				995											
GTC	TTG	CCG	CAG	GAC	AAA	GAA	TAC	TAC	AAA	GTA	AAG	GAG	CCA	GGG	GAA	3138			
Val	Leu	Pro	Gln	Asp	Lys	Glu	Tyr	Tyr	Lys	Val	Lys	Glu	Pro	Gly	Glu				
1000				1005				1010				1015							
AGC	CCC	ATA	TTC	TGG	TAC	GCA	CCT	GAA	TCC	TTG	ACG	GAG	AGC	AAG	TTT	3186			
Ser	Pro	Ile	Phe	Trp	Tyr	Ala	Pro	Glu	Ser	Leu	Thr	Glu	Ser	Lys	Phe				
				1020				1025				1030							

TCT GTG GCC TCA GAT GTG TGG AGC TTT GGA GTG GTT CTA TAC GAA CTT	3234
Ser Val Ala Ser Asp Val Trp Ser Phe Gly Val Val Leu Tyr Glu Leu	
1035 1040 1045	
TTC ACA TAC ATC GAG AAG AGT AAA AGT CCA CCC GTG GAA TTT ATG CGA	3282
Phe Thr Tyr Ile Glu Lys Ser Lys Ser Pro Pro Val Glu Phe Met Arg	
1050 1055 1060	
ATG ATT GGC AAT GAT AAA CAA GGG CAA ATG ATT GTG TTC CAT TTG ATA	3330
Met Ile Gly Asn Asp Lys Gln Gly Gln Met Ile Val Phe His Leu Ile	
1065 1070 1075	
GAG CTA CTG AAG AGC AAC GGA AGA TTG CCA AGG CCA GAA GGA TGC CCA	3378
Glu Leu Leu Lys Ser Asn Gly Arg Leu Pro Arg Pro Glu Gly Cys Pro	
1080 1085 1090 1095	
GAT GAG ATT TAT GTG ATC ATG ACA GAG TGC TGG AAC AAC AAT GTG AGC	3426
Asp Glu Ile Tyr Val Ile Met Thr Glu Cys Trp Asn Asn Asn Val Ser	
1100 1105 1110	
CAG CGT CCC TCC TTC AGG GAC CTT TCG TTC GGG TGG ATC AAA TCC GGG	3474
Gln Arg Pro Ser Phe Arg Asp Leu Ser Phe Gly Trp Ile Lys Ser Gly	
1115 1120 1125	
ACA GTA TAGCTGCGTG AAAGAGATGG CCTTCACTCA GAGACCAAGC AGACTTCCAG	3530
Thr Val	
AACCAGAACA AAGCTCTGTA GCCTTGTC TACACATCCT TATCATGATG CTAGCTAGGC	3590
AGAAGAAACT GTGACGCCGT CTGCTCAAAG CTTTGCTTC	3629

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1129 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Met Gly Met Ala Cys Leu Thr Met Thr Glu Met Glu Ala Thr Ser Thr	
1 5 10 15	
Ser Pro Val His Gln Asn Gly Asp Ile Pro Gly Ser Ala Asn Ser Val	
20 25 30	
Lys Gln Ile Glu Pro Val Leu Gln Val Tyr Leu Tyr His Ser Leu Gly	
35 40 45	
Gln Ala Glu Gly Glu Tyr Leu Lys Phe Pro Ser Gly Glu Tyr Val Ala	
50 55 60	
Glu Glu Ile Cys Val Ala Ala Ser Lys Ala Cys Gly Ile Thr Pro Val	
65 70 75 80	
Tyr His Asn Met Phe Ala Leu Met Ser Glu Thr Glu Arg Ile Trp Tyr	
85 90 95	
Pro Pro Asn His Val Phe His Ile Asp Glu Ser Thr Arg His Asp Ile	
100 105 110	

Leu Tyr Arg Ile Arg Phe Tyr Phe Pro His Trp Tyr Cys Ser Gly Ser
 115 120 125
 Ser Arg Thr Tyr Arg Tyr Gly Val Ser Arg Gly Ala Glu Ala Pro Leu
 130 135 140
 Leu Asp Asp Phe Val Met Ser Tyr Leu Phe Ala Gln Trp Arg His Asp
 145 150 155 160
 Phe Val His Gly Trp Ile Lys Val Pro Val Thr His Glu Thr Gln Glu
 165 170 175
 Glu Cys Leu Gly Met Ala Val Leu Asp Met Met Arg Ile Ala Lys Glu
 180 185 190
 Lys Asp Gln Thr Pro Leu Ala Val Tyr Asn Ser Val Ser Tyr Lys Thr
 195 200 205
 Phe Leu Pro Lys Cys Val Arg Ala Lys Ile Gln Asp Tyr His Ile Leu
 210 215 220
 Thr Arg Lys Arg Ile Arg Tyr Arg Phe Arg Arg Phe Ile Gln Gln Phe
 225 230 235 240
 Ser Gln Cys Lys Ala Thr Ala Arg Asn Leu Lys Leu Lys Tyr Leu Ile
 245 250 255
 Asn Leu Glu Thr Leu Gln Ser Ala Phe Tyr Thr Glu Gln Phe Glu Val
 260 265 270
 Lys Glu Ser Ala Arg Gly Pro Ser Gly Glu Glu Ile Phe Ala Thr Ile
 275 280 285
 Ile Ile Thr Gly Asn Gly Gly Ile Gln Trp Ser Arg Gly Lys His Lys
 290 295 300
 Glu Ser Glu Thr Leu Thr Glu Gln Asp Val Gln Leu Tyr Cys Asp Phe
 305 310 315 320
 Pro Asp Ile Ile Asp Val Ser Ile Lys Gln Ala Asn Gln Glu Cys Ser
 325 330 335
 Asn Glu Ser Arg Ile Val Thr Val His Lys Gln Asp Gly Lys Val Leu
 340 345 350
 Glu Ile Glu Leu Ser Ser Leu Lys Glu Ala Leu Ser Phe Val Ser Leu
 355 360 365
 Ile Asp Gly Tyr Tyr Arg Leu Thr Ala Asp Ala His His Tyr Leu Cys
 370 375 380
 Lys Glu Val Ala Pro Pro Ala Val Leu Glu Asn Ile His Ser Asn Cys
 385 390 395 400
 His Gly Pro Ile Ser Met Asp Phe Ala Ile Ser Lys Leu Lys Lys Ala
 405 410 415
 Gly Asn Gln Thr Gly Leu Tyr Val Leu Arg Cys Ser Pro Lys Asp Phe
 420 425 430
 Asn Lys Tyr Phe Leu Thr Phe Ala Val Glu Arg Glu Asn Val Ile Glu
 435 440 445

Tyr Lys His Cys Leu Ile Thr Lys Asn Glu Asn Gly Glu Tyr Asn Leu
450 455 460

Ser Gly Thr Lys Arg Asn Phe Ser Asn Leu Lys Asp Leu Leu Asn Cys
465 470 475 480

Tyr Gln Met Glu Thr Val Arg Ser Asp Ser Ile Ile Phe Gln Phe Thr
485 490 495

Lys Cys Cys Pro Pro Lys Pro Lys Asp Lys Ser Asn Leu Leu Val Phe
500 505 510

Arg Thr Asn Gly Ile Ser Asp Val Gln Ile Ser Pro Thr Leu Gln Arg
515 520 525

His Asn Asn Val Asn Gln Met Val Phe His Lys Ile Arg Asn Glu Asp
530 535 540

Leu Ile Phe Asn Glu Ser Leu Gly Gln Gly Thr Phe Thr Lys Ile Phe
545 550 555 560

Lys Gly Val Arg Arg Glu Val Gly Asp Tyr Gly Gln Leu His Lys Thr
565 570 575

Glu Val Leu Leu Lys Val Leu Asp Lys Ala His Arg Asn Tyr Ser Glu
580 585 590

Ser Phe Phe Glu Ala Ala Ser Met Met Ser Gln Leu Ser His Lys His
595 600 605

Leu Val Leu Asn Tyr Gly Val Cys Val Cys Gly Glu Glu Asn Ile Leu
610 615 620

Val Gln Glu Phe Val Lys Phe Gly Ser Leu Asp Thr Tyr Leu Lys Lys
625 630 635 640

Asn Lys Asn Ser Ile Asn Ile Leu Trp Lys Leu Gly Val Ala Lys Gln
645 650 655

Leu Ala Trp Ala Met His Phe Leu Glu Glu Lys Ser Leu Ile His Gly
660 665 670

Asn Val Cys Ala Lys Asn Ile Leu Leu Ile Arg Glu Glu Asp Arg Arg
675 680 685

Thr Gly Asn Pro Pro Phe Ile Lys Leu Ser Asp Pro Gly Ile Ser Ile
690 695 700

Thr Val Leu Pro Lys Asp Ile Leu Gln Glu Arg Ile Pro Trp Val Pro
705 710 715 720

Pro Glu Cys Ile Glu Asn Pro Lys Asn Leu Asn Leu Ala Thr Asp Lys
725 730 735

Trp Ser Phe Gly Thr Thr Leu Trp Glu Ile Cys Ser Gly Gly Asp Lys
740 745 750

Pro Leu Ser Ala Leu Asp Ser Gln Arg Lys Leu Gln Phe Tyr Glu Asp
755 760 765

Lys His Gln Leu Pro Ala Pro Lys Trp Thr Glu Leu Ala Asn Leu Ile
770 775 780

Asn	Asn	Cys	Met	Asp	Tyr	Glu	Pro	Asp	Phe	Arg	Pro	Ala	Phe	Arg	Ala	785	790	795	800
Val	Ile	Arg	Asp	Leu	Asn	Ser	Leu	Phe	Thr	Pro	Asp	Tyr	Glu	Leu	Leu	805	810	815	
Thr	Glu	Asn	Asp	Met	Leu	Pro	Asn	Met	Arg	Ile	Gly	Ala	Leu	Gly	Phe	820	825	830	
Ser	Gly	Ala	Phe	Glu	Asp	Arg	Asp	Pro	Thr	Gln	Phe	Glu	Glu	Arg	His	835	840	845	
Leu	Lys	Phe	Leu	Gln	Gln	Leu	Gly	Lys	Gly	Asn	Phe	Gly	Ser	Val	Glu	850	855	860	
Met	Cys	Arg	Tyr	Asp	Pro	Leu	Gln	Asp	Asn	Thr	Gly	Glu	Val	Val	Ala	865	870	875	880
Val	Lys	Lys	Leu	Gln	His	Ser	Thr	Glu	Glu	His	Leu	Arg	Asp	Phe	Glu	885	890	895	
Arg	Glu	Ile	Glu	Ile	Leu	Lys	Ser	Leu	Gln	His	Asp	Asn	Ile	Val	Lys	900	905	910	
Tyr	Lys	Gly	Val	Cys	Tyr	Ser	Ala	Gly	Arg	Arg	Asn	Leu	Arg	Leu	Ile	915	920	925	
Met	Glu	Tyr	Leu	Pro	Tyr	Gly	Ser	Leu	Arg	Asp	Tyr	Leu	Gln	Lys	His	930	935	940	
Lys	Glu	Arg	Ile	Asp	His	Lys	Lys	Leu	Leu	Gln	Tyr	Thr	Ser	Gln	Ile	945	950	955	960
Cys	Lys	Gly	Met	Glu	Tyr	Leu	Gly	Thr	Lys	Arg	Tyr	Ile	His	Arg	Asp	965	970	975	
Leu	Ala	Thr	Arg	Asn	Ile	Leu	Val	Glu	Asn	Glu	Asn	Arg	Val	Lys	Ile	980	985	990	
Gly	Asp	Phe	Gly	Leu	Thr	Lys	Val	Leu	Pro	Gln	Asp	Lys	Glu	Tyr	Tyr	995	1000	1005	
Lys	Val	Lys	Glu	Pro	Gly	Glu	Ser	Pro	Ile	Phe	Trp	Tyr	Ala	Pro	Glu	1010	1015	1020	
Ser	Leu	Thr	Glu	Ser	Lys	Phe	Ser	Val	Ala	Ser	Asp	Val	Trp	Ser	Phe	1025	1030	1035	1040
Gly	Val	Val	Leu	Tyr	Glu	Leu	Phe	Thr	Tyr	Ile	Glu	Lys	Ser	Lys	Ser	1045	1050	1055	
Pro	Pro	Val	Glu	Phe	Met	Arg	Met	Ile	Gly	Asn	Asp	Lys	Gln	Gly	Gln	1060	1065	1070	
Met	Ile	Val	Phe	His	Leu	Ile	Glu	Leu	Leu	Lys	Ser	Asn	Gly	Arg	Leu	1075	1080	1085	
Pro	Arg	Pro	Glu	Gly	Cys	Pro	Asp	Glu	Ile	Tyr	Val	Ile	Met	Thr	Glu	1090	1095	1100	
Cys	Trp	Asn	Asn	Asn	Val	Ser	Gln	Arg	Pro	Ser	Phe	Arg	Asp	Leu	Ser	1105	1110	1115	1120

Phe Gly Trp Ile Lys Ser Gly Thr Val
1125

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3429 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..3426

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

ATG GCT TTC TGT GCT AAA ATG AGG AGC TCC AAG AAG ACT GAG GTG AAC	48
Met Ala Phe Cys Ala Lys Met Arg Ser Ser Lys Lys Thr Glu Val Asn	
1 5 10 15	
CTG GAG GCC CCT GAG CCA GGG GTG GAA GTG ATC TTC TAT CTG TCG GAC	96
Leu Glu Ala Pro Glu Pro Gly Val Glu Val Ile Phe Tyr Leu Ser Asp	
20 25 30	
AGG GAG CCC CTC CGG CTG GGC AGT GGA GAG TAC ACA GCA GAG GAA CTG	144
Arg Glu Pro Leu Arg Leu Gly Ser Gly Glu Tyr Thr Ala Glu Glu Leu	
35 40 45	
TGC ATC AGG GCT GCA CAG GCA TGC CGT ATC TCT CCT CTT TGT CAC AAC	192
Cys Ile Arg Ala Ala Gln Ala Cys Arg Ile Ser Pro Leu Cys His Asn	
50 55 60	
CTC TTT GCC CTG TAT GAC GAG AAC ACC AAG CTC TGG TAT GCT CCA AAT	240
Leu Phe Ala Leu Tyr Asp Glu Asn Thr Lys Leu Trp Tyr Ala Pro Asn	
65 70 75 80	
CGC ACC ATC ACC GTT GAT GAC AAG ATG TCC CTC CGG CTC CAC TAC CGG	288
Arg Thr Ile Thr Val Asp Asp Lys Met Ser Leu Arg Leu His Tyr Arg	
85 90 95	
ATG AGG TTC TAT TTC ACC AAT TGG CAT GGA ACC AAC GAC AAT GAG CAG	336
Met Arg Phe Tyr Phe Thr Asn Trp His Gly Thr Asn Asp Asn Glu Gln	
100 105 110	
TCA GTG TGG CGT CAT TCT CCA AAG AAG CAG AAA AAT GGC TAC GAG AAA	384
Ser Val Trp Arg His Ser Pro Lys Lys Gln Lys Asn Gly Tyr Glu Lys	
115 120 125	
AAA AAG ATT CCA GAT GCA ACC CCT CTC CTT GAT GCC AGC TCA CTG GAG	432
Lys Lys Ile Pro Asp Ala Thr Pro Leu Leu Asp Ala Ser Ser Leu Glu	
130 135 140	
TAT CTG TTT GCT CAG GGA CAG TAT GAT TTG GTG AAA TGC CTG GCT CCT	480
Tyr Leu Phe Ala Gln Gly Gln Tyr Asp Leu Val Lys Cys Leu Ala Pro	
145 150 155 160	
ATT CGA GAC CCC AAG ACC GAG CAG GAT GGA CAT GAT ATT GAG AAC GAG	528
Ile Arg Asp Pro Lys Thr Glu Gln Asp Gly His Asp Ile Glu Asn Glu	
165 170 175	

TGT CTA GGG ATG GCT GTC CTG GCC ATC TCA CAC TAT GCC ATG ATG AAG Cys Leu Gly Met Ala Val Leu Ala Ile Ser His Tyr Ala Met Met Lys 180 185 190	576
AAG ATG CAG TTG CCA GAA CTG CCC AAG GAC ATC AGC TAC AAG CGA TAT Lys Met Gln Leu Pro Glu Leu Pro Lys Asp Ile Ser Tyr Lys Arg Tyr 195 200 205	624
ATT CCA GAA ACA TTG AAT AAG TCC ATC AGA CAG AGG AAC CTT CTC ACC Ile Pro Glu Thr Leu Asn Lys Ser Ile Arg Gln Asn Leu Leu Thr 210 215 220	672
AGG ATG CGG ATA AAT AAT GTT TTC AAG GAT TTC CTA AAG GAA TTT AAC Arg Met Arg Ile Asn Asn Val Phe Lys Asp Phe Leu Lys Glu Phe Asn 225 230 235 240	720
AAC AAG ACC ATT TGT GAC AGC AGC GTG TCC ACG CAT GAC CTG AAG GTG Asn Lys Thr Ile Cys Asp Ser Ser Val Ser Thr His Asp Leu Lys Val 245 250 255	768
AAA TAC TTG GCT ACC TTG GAA ACT TTG ACA AAA CAT TAC GGT GCT GAA Lys Tyr Leu Ala Thr Leu Glu Thr Leu Thr Lys His Tyr Gly Ala Glu 260 265 270	816
ATA TTT GAG ACT TCC ATG TTA CTG ATT TCA TCA GAA AAT GAG ATG AAT Ile Phe Glu Thr Ser Met Leu Leu Ile Ser Ser Glu Asn Glu Met Asn 275 280 285	864
TGG TTT CAT TCG AAT GAC GGT GGA AAC GTT CTC TAC TAC GAA GTG ATG Trp Phe His Ser Asn Asp Gly Gly Asn Val Leu Tyr Tyr Glu Val Met 290 295 300	912
GTG ACT GGG AAT CTT GGA ATC CAG TGG AGG CAT AAA CCA AAT GTT GTT Val Thr Gly Asn Leu Gln Ile Gln Trp Arg His Lys Pro Asn Val Val 305 310 315 320	960
TCT GTT GAA AAG GAA AAA AAT AAA CTG AAG CGG AAA AAA CTG GAA AAT Ser Val Glu Lys Glu Lys Asn Lys Leu Lys Arg Lys Lys Leu Glu Asn 325 330 335	1008
AAA GAC AAG AAG GAT GAG GAG AAA AAC AAG ATC CGG GAA GAG TGG AAC Lys Asp Lys Lys Asp Glu Glu Lys Asn Lys Ile Arg Glu Glu Trp Asn 340 345 350	1056
AAT TTT TCA TTC TTC CCT GAA ATC ACT CAC ATT GTA ATA AAG GAG TCT Asn Phe Ser Phe Phe Pro Glu Ile Thr His Ile Val Ile Lys Glu Ser 355 360 365	1104
GTG GTC AGC ATT AAC AAG CAG GAC AAC AAG AAA ATG GAA CTG AAG CTC Val Val Ser Ile Asn Lys Gln Asp Asn Lys Lys Met Glu Leu Lys Leu 370 375 380	1152
TCT TCC CAC GAG GAG GCC TTG TCC TTT GTG TCC CTG GTA GAT GGC TAC Ser Ser His Glu Glu Ala Leu Ser Phe Val Ser Leu Val Asp Gly Tyr 385 390 395 400	1200
TTC CGG CTC ACA GCA GAT GCC CAT CAT TAC CTC TGC ACC GAC GTG GCC Phe Arg Leu Thr Ala Asp Ala His His Tyr Leu Cys Thr Asp Val Ala 405 410 415	1248
CCC CCG TTG ATC GTC CAC AAC ATA CAG AAT GGC TGT CAT GGT CCA ATC Pro Pro Leu Ile Val His Asn Ile Gln Asn Gly Cys His Gly Pro Ile	1296

420	425	430	
TGT ACA GAA TAC GCC ATC AAT AAA TTG CGG CAA GAA GGA AGC GAG GAG Cys Thr Glu Tyr Ala Ile Asn Lys Leu Arg Gln Glu Gly Ser Glu Glu 435 440 445			1344
GGG ATG TAC GTG CTG AGG TGG AGC TGC ACC GAC TTT GAC AAC ATC CTC Gly Met Tyr Val Leu Arg Trp Ser Cys Thr Asp Phe Asp Asn Ile Leu 450 455 460			1392
ATG ACC GTC ACC TGC TTT GAG AAG TCT GAG CAG GTG CAG GGT GCC CAG Met Thr Val Thr Cys Phe Glu Lys Ser Glu Gln Val Gln Gly Ala Gln 465 470 475 480			1440
AAG CAG TTC AAG AAC TTT CAG ATC GAG GTG CAG AAG GGC CGC TAC AGT Lys Gln Phe Lys Asn Phe Gln Ile Glu Val Gln Lys Gly Arg Tyr Ser 485 490 495			1488
CTG CAC GGT TCG GAC CGC AGC TTC CCC AGC TTG GGA GAC CTC ATG AGC Leu His Gly Ser Asp Arg Ser Phe Pro Ser Leu Gly Asp Leu Met Ser 500 505 510			1536
CAC CTC AAG AAG CAG ATC CTG CGC ACG GAT AAC ATC AGC TTC ATG CTA His Leu Lys Lys Gln Ile Leu Arg Thr Asp Asn Ile Ser Phe Met Leu 515 520 525			1584
AAA CGC TGC TGC CAG CCC AAG CCC CGA GAA ATC TCC AAC CTG CTG GTG Lys Arg Cys Cys Gln Pro Lys Pro Arg Glu Ile Ser Asn Leu Leu Val 530 535 540			1632
GCT ACT AAG AAA GCC CAG GAG TGG CAG CCC GTC TAC CCC ATG AGC CAG Ala Thr Lys Lys Ala Gln Glu Trp Gln Pro Val Tyr Pro Met Ser Gln 545 550 555 560			1680
CTG AGT TTC GAT CGG ATC CTC AAG AAG GAT CTG GTG CAG GGC GAG CAC Leu Ser Phe Asp Arg Ile Leu Lys Lys Asp Leu Val Gln Gly Glu His 565 570 575			1728
CTT GGG AGA GGC ACG AGA ACA CAC ATC TAT TCT GGG ACC CTG ATG GAT Leu Gly Arg Gly Thr Arg Thr His Ile Tyr Ser Gly Thr Leu Met Asp 580 585 590			1776
TAC AAG GAT GAC GAA GGA ACT TCT GAA GAG AAG AAG ATA AAA GTG ATC Tyr Lys Asp Asp Glu Gly Thr Ser Glu Glu Lys Lys Ile Lys Val Ile 595 600 605			1824
CTC AAA GTC TTA GAC CCC AGC CAC AGG GAT ATT TCC CTG GCC TTC TTC Leu Lys Val Leu Asp Pro Ser His Arg Asp Ile Ser Leu Ala Phe Phe 610 615 620			1872
GAG GCA GCC AGC ATG ATG AGA CAG GTC TCC CAC AAA CAC ATC GTG TAC Glu Ala Ala Ser Met Met Arg Gln Val Ser His Lys His Ile Val Tyr 625 630 635 640			1920
CTC TAT GGC GTC TGT GTC CGC GAC GTG GAG AAT ATC ATG GTG GAA GAG Leu Tyr Gly Val Cys Val Arg Asp Val Glu Asn Ile Met Val Glu Glu 645 650 655			1968
TTT GTG GAA GGG GGT CCT CTG GAT CTC TTC ATG CAC CGG AAA AGT GAT Phe Val Glu Gly Gly Pro Leu Asp Leu Phe Met His Arg Lys Ser Asp 660 665 670			2016

GTC	CTT	ACC	ACA	CCA	TGG	AAA	TTC	AAA	GTT	GCC	AAA	CAG	CTG	GCC	AGT	2064
Val	Leu	Thr	Thr	Pro	Trp	Lys	Phe	Lys	Val	Ala	Lys	Gln	Leu	Ala	Ser	
		675					680					685				
GCC	CTG	AGC	TAC	TTG	GAG	GAT	AAA	GAC	CTG	GTC	CAT	GGA	AAT	GTG	TGT	2112
Ala	Leu	Ser	Tyr	Leu	Glu	Asp	Lys	Asp	Leu	Val	His	Gly	Asn	Val	Cys	
	690					695					700					
ACT	AAA	AAC	CTC	CTC	CTG	GCC	CGT	GAG	GGA	ATC	GAC	AGT	GAG	TGT	GGC	2160
Thr	Lys	Asn	Leu	Leu	Leu	Ala	Arg	Glu	Gly	Ile	Asp	Ser	Glu	Cys	Gly	
705					710					715					720	
CCA	TTC	ATC	AAG	CTC	AGT	GAC	CCC	GGC	ATC	CCC	ATT	ACG	GTG	CTG	TCT	2208
Pro	Phe	Ile	Lys		Leu	Ser	Asp	Pro	Gly	Ile	Pro	Ile	Thr	Val	Leu	Ser
				725					730						735	
AGG	CAA	GAA	TGC	ATT	GAA	CGA	ATC	CCA	TGG	ATT	GCT	CCT	GAG	TGT	GTT	2256
Arg	Gln	Glu	Cys	Ile	Glu	Arg	Ile	Pro	Trp	Ile	Ala	Pro	Glu	Cys	Val	
			740					745					750			
GAG	GAC	TCC	AAG	AAC	CTG	AGT	GTG	GCT	GCT	GAC	AAG	TGG	AGC	TTT	GGA	2304
Glu	Asp	Ser	Lys	Asn	Leu	Ser	Val	Ala	Ala	Asp	Lys	Trp	Ser	Phe	Gly	
		755					760					765				
ACC	ACG	CTC	TGG	GAA	ATC	TGC	TAC	AAT	GGC	GAG	ATC	CCC	TTG	AAA	GAC	2352
Thr	Thr	Leu	Trp	Glu	Ile	Cys	Tyr	Asn	Gly	Glu	Ile	Pro	Leu	Lys	Asp	
	770					775					780					
AAG	ACG	CTG	ATT	GAG	AAA	GAG	AGA	TTC	TAT	GAA	AGC	CGG	TGC	AGG	CCA	2400
Lys	Thr	Leu	Ile	Glu	Lys	Glu	Arg	Phe	Tyr	Glu	Ser	Arg	Cys	Arg	Pro	
785					790					795					800	
GTG	ACA	CCA	TCA	TGT	AAG	GAG	CTG	GCT	GAC	CTC	ATG	ACC	CGC	TGC	ATG	2448
Val	Thr	Pro	Ser	Cys	Lys	Glu	Leu	Ala	Asp	Leu	Met	Thr	Arg	Cys	Met	
				805					810						815	
AAC	TAT	GAC	CCC	AAT	CAG	AGG	CCT	TTC	TTC	CGA	GCC	ATC	ATG	AGA	GAC	2496
Asn	Tyr	Asp		Pro	Asn	Gln	Arg	Pro	Phe	Phe	Arg	Ala	Ile	Met	Arg	Asp
			820						825					830		
ATT	AAT	AAG	CTT	GAA	GAG	CAG	AAT	CCA	GAT	ATT	GTT	TCC	AGA	AAA	AAA	2544
Ile	Asn	Lys	Leu	Glu	Glu	Gln	Asn	Pro	Asp	Ile	Val	Ser	Arg	Lys	Lys	
		835					840					845				
AAC	CAG	CCA	ACT	GAA	GTG	GAC	CCC	ACA	CAT	TTT	GAG	AAG	CGC	TTC	CTA	2592
Asn	Gln	Pro	Thr	Glu	Val	Asp	Pro	Thr	His	Phe	Glu	Lys	Arg	Phe	Leu	
	850					855					860					
AAG	AGG	ATC	CGT	GAC	TTG	GGA	GAG	GGC	CAC	TTT	GGG	AAG	GTT	GAG	CTC	2640
Lys	Arg	Ile	Arg	Asp	Leu	Gly	Glu	Gly	His	Phe	Gly	Lys	Val	Glu	Leu	
865					870					875					880	
TGC	AGG	TAT	GAC	CCC	GAA	GAC	AAT	ACA	GGG	GAG	CAG	GTG	GCT	GTT	AAA	2688
Cys	Arg	Tyr	Asp	Pro	Glu	Asp	Asn	Thr	Gly	Glu	Gln	Val	Ala	Val	Lys	
				885					890						895	
TCT	CTG	AAG	CCT	GAG	AGT	GGA	GGT	AAC	CAC	ATA	GCT	GAT	CTG	AAA	AAG	2736
Ser	Leu	Lys	Pro	Glu	Ser	Gly	Gly	Asn	His	Ile	Ala	Asp	Leu	Lys	Lys	
			900					905					910			
GAA	ATC	GAG	ATC	TTA	AGG	AAC	CTC	TAT	CAT	GAG	AAC	ATT	GTG	AAG	TAC	2784

Glu	Ile	Glu	Ile	Leu	Arg	Asn	Leu	Tyr	His	Glu	Asn	Ile	Val	Lys	Tyr	
		915					920					925				
AAA	GGA	ATC	TGC	ACA	GAA	GAC	GGA	GGA	AAT	GGT	ATT	AAG	CTC	ATC	ATG	2832
Lys	Gly	Ile	Cys	Thr	Glu	Asp	Gly	Gly	Asn	Gly	Ile	Lys	Leu	Ile	Met	
		930				935					940					
GAA	TTT	CTG	CCT	TCG	GGA	AGC	CTT	AAG	GAA	TAT	CTT	CCA	AAG	AAT	AAG	2880
Glu	Phe	Leu	Pro	Ser	Gly	Ser	Leu	Lys	Glu	Tyr	Leu	Pro	Lys	Asn	Lys	
		945				950				955					960	
AAC	AAA	ATA	AAC	CTC	AAA	CAG	CAG	CTA	AAA	TAT	GCC	GTT	CAG	ATT	TGT	2928
Asn	Lys	Ile	Asn	Leu	Lys	Gln	Gln	Leu	Lys	Tyr	Ala	Val	Gln	Ile	Cys	
				965					970					975		
AAG	GGG	ATG	GAC	TAT	TTG	GGT	TCT	CGG	CAA	TAC	GTT	CAC	CGG	GAC	TTG	2976
Lys	Gly	Met	Asp	Tyr	Leu	Gly	Ser	Arg	Gln	Tyr	Val	His	Arg	Asp	Leu	
			980					985					990			
GCA	GCA	AGA	AAT	GTC	CTT	GTT	GAG	AGT	GAA	CAC	CAA	GTG	AAA	ATT	GGA	3024
Ala	Ala	Arg	Asn	Val	Leu	Val	Glu	Ser	Glu	His	Gln	Val	Lys	Ile	Gly	
		995					1000					1005				
GAC	TTC	GGT	TTA	ACC	AAA	GCA	ATT	GAA	ACC	GAT	AAG	GAG	TAT	TAC	ACC	3072
Asp	Phe	Gly	Leu	Thr	Lys	Ala	Ile	Glu	Thr	Asp	Lys	Glu	Tyr	Tyr	Thr	
	1010					1015					1020					
GTC	AAG	GAT	GAC	CGG	GAC	AGC	CCT	GTG	TTT	TGG	TAT	GCT	CCA	GAA	TGT	3120
Val	Lys	Asp	Asp	Arg	Asp	Ser	Pro	Val	Phe	Trp	Tyr	Ala	Pro	Glu	Cys	
	1025				1030					1035					1040	
TTA	ATG	CAA	TCT	AAA	TTT	TAT	ATT	GCC	TCT	GAC	GTC	TGG	TCT	TTT	GGA	3168
Leu	Met	Gln	Ser	Lys	Phe	Tyr	Ile	Ala	Ser	Asp	Val	Trp	Ser	Phe	Gly	
				1045				1050						1055		
GTC	ACT	CTG	CAT	GAG	CTG	CTG	ACT	TAC	TGT	GAT	TCA	GAT	TCT	AGT	CCC	3216
Val	Thr	Leu	His	Glu	Leu	Leu	Thr	Tyr	Cys	Asp	Ser	Asp	Ser	Ser	Pro	
			1060					1065					1070			
ATG	GCT	TTG	TTC	CTG	AAA	ATG	ATA	GGC	CCA	ACC	CAT	GGC	CAG	ATG	ACA	3264
Met	Ala	Leu	Phe	Leu	Lys	Met	Ile	Gly	Pro	Thr	His	Gly	Gln	Met	Thr	
		1075					1080					1085				
GTC	ACA	AGA	CTT	GTG	AAT	ACG	TTA	AAA	GAA	GGA	AAA	CGC	CTG	CCG	TGC	3312
Val	Thr	Arg	Leu	Val	Asn	Thr	Leu	Lys	Glu	Gly	Lys	Arg	Leu	Pro	Cys	
	1090					1095					1100					
CCA	CCT	AAC	TGT	CCA	GAT	GAG	GTT	TAT	CAG	CTT	ATG	AGA	AAA	TGC	TGG	3360
Pro	Pro	Asn	Cys	Pro	Asp	Glu	Val	Tyr	Gln	Leu	Met	Arg	Lys	Cys	Trp	
	1105				1110				1115					1120		
GAA	TTC	CAA	CCA	TCC	AAT	CGG	ACA	AGC	TTT	CAG	AAC	CTT	ATT	GAA	GGA	3408
Glu	Phe	Gln	Pro	Ser	Asn	Arg	Thr	Ser	Phe	Gln	Asn	Leu	Ile	Glu	Gly	
				1125				1130						1135		
TTT	GAA	GCA	CTT	TTA	AAA	TAA										3429
Phe	Glu	Ala	Leu	Leu	Lys											
				1140												

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1142 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

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Met Ala Phe Cys Ala Lys Met Arg Ser Ser Lys Lys Thr Glu Val Asn
 1           5           10           15
Leu Glu Ala Pro Glu Pro Gly Val Glu Val Ile Phe Tyr Leu Ser Asp
          20           25           30
Arg Glu Pro Leu Arg Leu Gly Ser Gly Glu Tyr Thr Ala Glu Glu Leu
          35           40           45
Cys Ile Arg Ala Ala Gln Ala Cys Arg Ile Ser Pro Leu Cys His Asn
          50           55           60
Leu Phe Ala Leu Tyr Asp Glu Asn Thr Lys Leu Trp Tyr Ala Pro Asn
          65           70           75           80
Arg Thr Ile Thr Val Asp Asp Lys Met Ser Leu Arg Leu His Tyr Arg
          85           90           95
Met Arg Phe Tyr Phe Thr Asn Trp His Gly Thr Asn Asp Asn Glu Gln
          100          105          110
Ser Val Trp Arg His Ser Pro Lys Lys Gln Lys Asn Gly Tyr Glu Lys
          115          120          125
Lys Lys Ile Pro Asp Ala Thr Pro Leu Leu Asp Ala Ser Ser Leu Glu
          130          135          140
Tyr Leu Phe Ala Gln Gly Gln Tyr Asp Leu Val Lys Cys Leu Ala Pro
          145          150          155          160
Ile Arg Asp Pro Lys Thr Glu Gln Asp Gly His Asp Ile Glu Asn Glu
          165          170          175
Cys Leu Gly Met Ala Val Leu Ala Ile Ser His Tyr Ala Met Met Lys
          180          185          190
Lys Met Gln Leu Pro Glu Leu Pro Lys Asp Ile Ser Tyr Lys Arg Tyr
          195          200          205
Ile Pro Glu Thr Leu Asn Lys Ser Ile Arg Gln Arg Asn Leu Leu Thr
          210          215          220
Arg Met Arg Ile Asn Asn Val Phe Lys Asp Phe Leu Lys Glu Phe Asn
          225          230          235          240
Asn Lys Thr Ile Cys Asp Ser Ser Val Ser Thr His Asp Leu Lys Val
          245          250          255
Lys Tyr Leu Ala Thr Leu Glu Thr Leu Thr Lys His Tyr Gly Ala Glu
          260          265          270
Ile Phe Glu Thr Ser Met Leu Leu Ile Ser Ser Glu Asn Glu Met Asn
          275          280          285

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Trp	Phe	His	Ser	Asn	Asp	Gly	Gly	Asn	Val	Leu	Tyr	Tyr	Glu	Val	Met
290						295					300				
Val	Thr	Gly	Asn	Leu	Gly	Ile	Gln	Trp	Arg	His	Lys	Pro	Asn	Val	Val
305					310					315					320
Ser	Val	Glu	Lys	Glu	Lys	Asn	Lys	Leu	Lys	Arg	Lys	Lys	Leu	Glu	Asn
				325					330					335	
Lys	Asp	Lys	Lys	Asp	Glu	Glu	Lys	Asn	Lys	Ile	Arg	Glu	Glu	Trp	Asn
			340					345					350		
Asn	Phe	Ser	Phe	Phe	Pro	Glu	Ile	Thr	His	Ile	Val	Ile	Lys	Glu	Ser
		355					360					365			
Val	Val	Ser	Ile	Asn	Lys	Gln	Asp	Asn	Lys	Lys	Met	Glu	Leu	Lys	Leu
370						375					380				
Ser	Ser	His	Glu	Glu	Ala	Leu	Ser	Phe	Val	Ser	Leu	Val	Asp	Gly	Tyr
385					390					395					400
Phe	Arg	Leu	Thr	Ala	Asp	Ala	His	His	Tyr	Leu	Cys	Thr	Asp	Val	Ala
				405					410					415	
Pro	Pro	Leu	Ile	Val	His	Asn	Ile	Gln	Asn	Gly	Cys	His	Gly	Pro	Ile
			420					425					430		
Cys	Thr	Glu	Tyr	Ala	Ile	Asn	Lys	Leu	Arg	Gln	Glu	Gly	Ser	Glu	Glu
		435					440					445			
Gly	Met	Tyr	Val	Leu	Arg	Trp	Ser	Cys	Thr	Asp	Phe	Asp	Asn	Ile	Leu
450						455					460				
Met	Thr	Val	Thr	Cys	Phe	Glu	Lys	Ser	Glu	Gln	Val	Gln	Gly	Ala	Gln
465					470					475					480
Lys	Gln	Phe	Lys	Asn	Phe	Gln	Ile	Glu	Val	Gln	Lys	Gly	Arg	Tyr	Ser
				485					490					495	
Leu	His	Gly	Ser	Asp	Arg	Ser	Phe	Pro	Ser	Leu	Gly	Asp	Leu	Met	Ser
			500					505					510		
His	Leu	Lys	Lys	Gln	Ile	Leu	Arg	Thr	Asp	Asn	Ile	Ser	Phe	Met	Leu
		515					520					525			
Lys	Arg	Cys	Cys	Gln	Pro	Lys	Pro	Arg	Glu	Ile	Ser	Asn	Leu	Leu	Val
	530					535					540				
Ala	Thr	Lys	Lys	Ala	Gln	Glu	Trp	Gln	Pro	Val	Tyr	Pro	Met	Ser	Gln
545					550					555					560
Leu	Ser	Phe	Asp	Arg	Ile	Leu	Lys	Lys	Asp	Leu	Val	Gln	Gly	Glu	His
				565					570					575	
Leu	Gly	Arg	Gly	Thr	Arg	Thr	His	Ile	Tyr	Ser	Gly	Thr	Leu	Met	Asp
		580					585						590		
Tyr	Lys	Asp	Asp	Glu	Gly	Thr	Ser	Glu	Glu	Lys	Lys	Ile	Lys	Val	Ile
		595					600					605			
Leu	Lys	Val	Leu	Asp	Pro	Ser	His	Arg	Asp	Ile	Ser	Leu	Ala	Phe	Phe
610						615					620				

Glu Ala Ala Ser Met Met Arg Gln Val Ser His Lys His Ile Val Tyr
625 630 635 640

Leu Tyr Gly Val Cys Val Arg Asp Val Glu Asn Ile Met Val Glu Glu
645 650 655

Phe Val Glu Gly Gly Pro Leu Asp Leu Phe Met His Arg Lys Ser Asp
660 665 670

Val Leu Thr Thr Pro Trp Lys Phe Lys Val Ala Lys Gln Leu Ala Ser
675 680 685

Ala Leu Ser Tyr Leu Glu Asp Lys Asp Leu Val His Gly Asn Val Cys
690 695 700

Thr Lys Asn Leu Leu Leu Ala Arg Glu Gly Ile Asp Ser Glu Cys Gly
705 710 715 720

Pro Phe Ile Lys Leu Ser Asp Pro Gly Ile Pro Ile Thr Val Leu Ser
725 730 735

Arg Gln Glu Cys Ile Glu Arg Ile Pro Trp Ile Ala Pro Glu Cys Val
740 745 750

Glu Asp Ser Lys Asn Leu Ser Val Ala Ala Asp Lys Trp Ser Phe Gly
755 760 765

Thr Thr Leu Trp Glu Ile Cys Tyr Asn Gly Glu Ile Pro Leu Lys Asp
770 775 780

Lys Thr Leu Ile Glu Lys Glu Arg Phe Tyr Glu Ser Arg Cys Arg Pro
785 790 795 800

Val Thr Pro Ser Cys Lys Glu Leu Ala Asp Leu Met Thr Arg Cys Met
805 810 815

Asn Tyr Asp Pro Asn Gln Arg Pro Phe Phe Arg Ala Ile Met Arg Asp
820 825 830

Ile Asn Lys Leu Glu Glu Gln Asn Pro Asp Ile Val Ser Arg Lys Lys
835 840 845

Asn Gln Pro Thr Glu Val Asp Pro Thr His Phe Glu Lys Arg Phe Leu
850 855 860

Lys Arg Ile Arg Asp Leu Gly Glu Gly His Phe Gly Lys Val Glu Leu
865 870 875 880

Cys Arg Tyr Asp Pro Glu Asp Asn Thr Gly Glu Gln Val Ala Val Lys
885 890 895

Ser Leu Lys Pro Glu Ser Gly Gly Asn His Ile Ala Asp Leu Lys Lys
900 905 910

Glu Ile Glu Ile Leu Arg Asn Leu Tyr His Glu Asn Ile Val Lys Tyr
915 920 925

Lys Gly Ile Cys Thr Glu Asp Gly Gly Asn Gly Ile Lys Leu Ile Met
930 935 940

Glu Phe Leu Pro Ser Gly Ser Leu Lys Glu Tyr Leu Pro Lys Asn Lys
945 950 955 960

Asn Lys Ile Asn Leu Lys Gln Gln Leu Lys Tyr Ala Val Gln Ile Cys
965 970 975

Lys Gly Met Asp Tyr Leu Gly Ser Arg Gln Tyr Val His Arg Asp Leu
980 985 990

Ala Ala Arg Asn Val Leu Val Glu Ser Glu His Gln Val Lys Ile Gly
995 1000 1005

Asp Phe Gly Leu Thr Lys Ala Ile Glu Thr Asp Lys Glu Tyr Tyr Thr
1010 1015 1020

Val Lys Asp Asp Arg Asp Ser Pro Val Phe Trp Tyr Ala Pro Glu Cys
1025 1030 1035 1040

Leu Met Gln Ser Lys Phe Tyr Ile Ala Ser Asp Val Trp Ser Phe Gly
1045 1050 1055

Val Thr Leu His Glu Leu Leu Thr Tyr Cys Asp Ser Asp Ser Ser Pro
1060 1065 1070

Met Ala Leu Phe Leu Lys Met Ile Gly Pro Thr His Gly Gln Met Thr
1075 1080 1085

Val Thr Arg Leu Val Asn Thr Leu Lys Glu Gly Lys Arg Leu Pro Cys
1090 1095 1100

Pro Pro Asn Cys Pro Asp Glu Val Tyr Gln Leu Met Arg Lys Cys Trp
1105 1110 1115 1120

Glu Phe Gln Pro Ser Asn Arg Thr Ser Phe Gln Asn Leu Ile Glu Gly
1125 1130 1135

Phe Glu Ala Leu Leu Lys
1140

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3561 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..3561

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

ATG CCT CTG CGC CAC TGG GGG ATG GCC AGG GGC AGT AAG CCC GTT GGG	48
Met Pro Leu Arg His Trp Gly Met Ala Arg Gly Ser Lys Pro Val Gly	
1 5 10 15	
GAT GGA GCC CAG CCC ATG GCT GCC ATG GGA GGC CTG AAG GTG CTT CTG	96
Asp Gly Ala Gln Pro Met Ala Ala Met Gly Gly Leu Lys Val Leu Leu	
20 25 30	
CAC TGG GCT GGT CCA GGC GGC GGG GAG CCC TGG GTC ACT TTC AGT GAG	144
His Trp Ala Gly Pro Gly Gly Gly Glu Pro Trp Val Thr Phe Ser Glu	

35	40	45	
TCA TCG CTG ACA GCT GAG GAA GTC TGC ATC CAC ATT GCA CAT AAA GTT Ser Ser Leu Thr Ala Glu Glu Val Cys Ile His Ile Ala His Lys Val 50 55 60			192
GGT ATC ACT CCT CCT TGC TTC AAT CTC TTT GCC CTC TTC GAT GCT CAG Gly Ile Thr Pro Pro Cys Phe Asn Leu Phe Ala Leu Phe Asp Ala Gln 65 70 75 80			240
GCC CAA GTC TGG TTG CCC CCA AAC CAC ATC CTA GAG ATC CCC AGA GAT Ala Gln Val Trp Leu Pro Pro Asn His Ile Leu Glu Ile Pro Arg Asp 85 90 95			288
GCA AGC CTG ATG CTA TAT TTC CGC ATA AGG TTT TAT TTC CGG AAC TGG Ala Ser Leu Met Leu Tyr Phe Arg Ile Arg Phe Tyr Phe Asn Trp 100 105 110			336
CAT GGC ATG AAT CCT CGG GAA CCG GCT GTG TAC CGT TGT GGG CCC CCA His Gly Met Asn Pro Arg Glu Pro Ala Val Tyr Arg Cys Gly Pro Pro 115 120 125			384
GGA ACC GAG GCA TCC TCA GAT CAG ACA GCA CAG GGG ATG CAA CTC CTG Gly Thr Glu Ala Ser Ser Asp Gln Thr Ala Gln Gly Met Gln Leu Leu 130 135 140			432
GAC CCA GCC TCA TTT GAG TAC CTC TTT GAG CAG GGC AAG CAT GAG TTT Asp Pro Ala Ser Phe Glu Tyr Leu Phe Glu Gln Gly Lys His Glu Phe 145 150 155 160			480
GTG AAT GAC GTG GCA TCA CTG TGG GAG CTG TCG ACC GAG GAG GAG ATC Val Asn Asp Val Ala Ser Leu Trp Glu Leu Ser Thr Glu Glu Glu Ile 165 170 175			528
CAC CAC TTT AAG AAT GAG AGC CTG GGC ATG GCC TTT CTG CAC CTC TGT His His Phe Lys Asn Glu Ser Leu Gly Met Ala Phe Leu His Leu Cys 180 185 190			576
CAC CTC GCT CTC CGC CAT GGC ATC CCC CTG GAG GAG GTG GCC AAG AAG His Leu Ala Leu Arg His Gly Ile Pro Leu Glu Glu Val Ala Lys Lys 195 200 205			624
ACC AGC TTC AAG GAC TGC ATC CCG CGC TCC TTC CGC CGG CAT ATC CGG Thr Ser Phe Lys Asp Cys Ile Pro Arg Ser Phe Arg Arg His Ile Arg 210 215 220			672
CAG CAC AGC GCC CTG ACC CGG CTG CGC CTT CGG AAC GTC TTC CGC AGG Gln His Ser Ala Leu Thr Arg Leu Arg Leu Arg Asn Val Phe Arg Arg 225 230 235 240			720
TTC CTG CGG GAC TTC CAG CCG GGC CGA CTC TCC CAG CAG ATG GTC ATG Phe Leu Arg Asp Phe Gln Pro Gly Arg Leu Ser Gln Gln Met Val Met 245 250 255			768
GTC AAA TAC CTA GCC ACA CTC GAG CGG CTG GCA CCC CGC TTC GGC ACA Val Lys Tyr Leu Ala Thr Leu Glu Arg Leu Ala Pro Arg Phe Gly Thr 260 265 270			816
GAG CGT GTG CCC GTG TGC CAC CTG AGG CTG CTG GCC CAG GCC GAG GGG Glu Arg Val Pro Val Cys His Leu Arg Leu Leu Ala Gln Ala Glu Gly 275 280 285			864

GAG CCC TGC TAC ATC CGG GAC AGT GGG GTG GCC CCT ACA GAC CCT GGC Glu Pro Cys Tyr Ile Arg Asp Ser Gly Val Ala Pro Thr Asp Pro Gly 290 295 300	912
CCT GAG TCT GCT GCT GGG CCC CCA ACC CAC GAG GTG CTG GTG ACA GGC Pro Glu Ser Ala Ala Gly Pro Pro Thr His Glu Val Leu Val Thr Gly 305 310 315 320	960
ACT GGT GGC ATC CAG TGG TGG CCA GTA GAG GAG GAG GTG AAC AAG GAG Thr Gly Gly Ile Gln Trp Trp Pro Val Glu Glu Val Asn Lys Glu 325 330 335	1008
GAG GGT TCT AGT GGC AGC AGT GGC AGG AAC CCC CAA GCC AGC CTG TTT Glu Gly Ser Ser Gly Ser Ser Gly Arg Asn Pro Gln Ala Ser Leu Phe 340 345 350	1056
GGG AAG AAG GCC AAG GCT CAC AAG GCA TTC GGC CAG CCG GCA GAC AGG Gly Lys Lys Ala Lys Ala His Lys Ala Phe Gly Gln Pro Ala Asp Arg 355 360 365	1104
CCG CGG GAG CCA CTG TGG GCC TAC TTC TGT GAC TTC CGG GAC ATC ACC Pro Arg Glu Pro Leu Trp Ala Tyr Phe Cys Asp Phe Arg Asp Ile Thr 370 375 380	1152
CAC GTG GTG CTG AAA GAG CAC TGT GTC AGC ATC CAC CGG CAG GAC AAC His Val Val Leu Lys Glu His Cys Val Ser Ile His Arg Gln Asp Asn 385 390 395 400	1200
AAG TGC CTG GAG CTG AGC TTG CCT TCC CGG GCT GCG GCG CTG TCC TTC Lys Cys Leu Glu Leu Ser Leu Pro Ser Arg Ala Ala Ala Leu Ser Phe 405 410 415	1248
GTG TCG CTG GTG GAC GGC TAT TTC CGC CTG ACG GCC GAC TCC AGC CAC Val Ser Leu Val Asp Gly Tyr Phe Arg Leu Thr Ala Asp Ser Ser His 420 425 430	1296
TAC CTG TGC CAC GAG GTG GCT CCC CCA CGG CTG GTG ATG AGC ATC CGG Tyr Leu Cys His Glu Val Ala Pro Pro Arg Leu Val Met Ser Ile Arg 435 440 445	1344
GAT GGG ATC CAC GGA CCC CTG CTG GAG CCA TTT GTG CAG GCC AAG CTG Asp Gly Ile His Gly Pro Leu Leu Glu Pro Phe Val Gln Ala Lys Leu 450 455 460	1392
CGG CCC GAG GAC GGC CTG TAC CTC ATT CAC TGG AGC ACC AGC CAC CCC Arg Pro Glu Asp Gly Leu Tyr Leu Ile His Trp Ser Thr Ser His Pro 465 470 475 480	1440
TAC CGC CTG ATC CTC ACA GTG GCC CAG CGT AGC CAG GCA CCA GAC GGC Tyr Arg Leu Ile Leu Thr Val Ala Gln Arg Ser Gln Ala Pro Asp Gly 485 490 495	1488
ATG CAG AGC TTG CGG CTC CGA AAG TTC CCC ATT GAG CAG CAG GAC GGG Met Gln Ser Leu Arg Leu Arg Lys Phe Pro Ile Glu Gln Gln Asp Gly 500 505 510	1536
GCC TTC GTG CTG GAG GGC TGG GGC CGG TCC TTC CCC AGC GTT CGG GAA Ala Phe Val Leu Glu Gly Trp Gly Arg Ser Phe Pro Ser Val Arg Glu 515 520 525	1584
CTT GGG GCT GCC TTG CAG GGC TGC TTG CTG AGG GCC GGG GAT GAC TGC Leu Gly Ala Ala Leu Gln Gly Cys Leu Leu Arg Ala Gly Asp Asp Cys	1632

530	535	540	
TTC TCT CTG CGT CGC TGT TGC CTG CCC CAA CCA GGA GAA ACC TCC AAT			1680
Phe Ser Leu Arg Arg Cys Leu Pro Gln Pro Gly Glu Thr Ser Asn			
545	550	555	560
CTC ATC ATC ATG CGG GGG GCT CGG GCC AGC CCC AGG ACA CTC AAC CTC			1728
Leu Ile Ile Met Arg Gly Ala Arg Ala Ser Pro Arg Thr Leu Asn Leu			
	565	570	575
AGC CAG CTC AGC TTC CAC CGG GTT GAC CAG AAG GAG ATC ACC CAG CTG			1776
Ser Gln Leu Ser Phe His Arg Val Asp Gln Lys Glu Ile Thr Gln Leu			
	580	585	590
TCC CAC TTG GGC CAG GGC ACA AGG ACC AAC GTG TAT GAG GGC CGC CTG			1824
Ser His Leu Gly Gln Gly Thr Arg Thr Asn Val Tyr Glu Gly Arg Leu			
	595	600	605
CGA GTG GAG GGC AGC GGG GAC CCT GAG GAG GGC AAG ATG GAT GAC GAG			1872
Arg Val Glu Gly Ser Gly Asp Pro Glu Glu Gly Lys Met Asp Asp Glu			
	610	615	620
GAC CCC CTC GTG CCT GGC AGG GAC CGT GGG CAG GAG CTA CGA GTG GTG			1920
Asp Pro Leu Val Pro Gly Arg Asp Arg Gly Gln Glu Leu Arg Val Val			
	625	630	635
CTC AAA GTG CTG GAC CCT AGT CAC CAT GAC ATC GCC CTG GCC TTC TAC			1968
Leu Lys Val Leu Asp Pro Ser His His Asp Ile Ala Leu Ala Phe Tyr			
	645	650	655
GAG ACA GCC AGC CTC ATG AGC CAG GTC TCC CAC ACG CAC CTG GCC TTC			2016
Glu Thr Ala Ser Leu Met Ser Gln Val Ser His Thr His Leu Ala Phe			
	660	665	670
GTG CAT GGC GTC TGT GTG CGC GGC CCT GAA AAT AGC ATG GTG ACA GAG			2064
Val His Gly Val Cys Val Arg Gly Pro Glu Asn Ser Met Val Thr Glu			
	675	680	685
TAC GTG GAG CAC GGA CCC CTG GAT GTG TGG CTG CGG AGG GAG CGG GGC			2112
Tyr Val Glu His Gly Pro Leu Asp Val Trp Leu Arg Arg Glu Arg Gly			
	690	695	700
CAT GTG CCC ATG GCT TGG AAG ATG GTG GTG GCC CAG CAG CTG GCC AGC			2160
His Val Pro Met Ala Trp Lys Met Val Val Ala Gln Gln Leu Ala Ser			
	705	710	715
GCC CTC AGC TAC CTG GAG AAC AAG AAC CTG GTT CAT GGT AAT GTG TGT			2208
Ala Leu Ser Tyr Leu Glu Asn Lys Asn Leu Val His Gly Asn Val Cys			
	725	730	735
GGC CGG AAC ATC CTG CTG GCC CGG CTG GGG TTG GCA GAG GGC ACC AGC			2256
Gly Arg Asn Ile Leu Leu Ala Arg Leu Gly Leu Ala Glu Gly Thr Ser			
	740	745	750
CCC TTC ATC AAG CTG AGT GAT CCT GGC GTG GGC CTG GGC GCC CTC TCC			2304
Pro Phe Ile Lys Leu Ser Asp Pro Gly Val Gly Leu Gly Ala Leu Ser			
	755	760	765
AGG GAG GAG CGG GTG GAG AGG ATC CCC TGG CTG GCC CCC GAA TGC CTA			2352
Arg Glu Glu Arg Val Glu Arg Ile Pro Trp Leu Ala Pro Glu Cys Leu			
	770	775	780

CCA GGT GGG GCC AAC AGC CTA AGC ACC GCC ATG GAC AAG TGG GGG TTT Pro Gly Gly Ala Asn Ser Leu Ser Thr Ala Met Asp Lys Trp Gly Phe 785 790 795 800	2400
GGC GCC ACC CTC CTG GAG ATC TGC TTT GAC GGA GAG GCC CCT CTG CAG Gly Ala Thr Leu Leu Glu Ile Cys Phe Asp Gly Glu Ala Pro Leu Gln 805 810 815	2448
AGC CGC AGT CCC TCC GAG AAG GAG CAT TTC TAC CAG AGG CAG CAC CGG Ser Arg Ser Pro Ser Glu Lys Glu His Phe Tyr Gln Arg Gln His Arg 820 825 830	2496
CTG CCC GAG CCC TCC TGC CCA CAG CTG GCC ACA CTC ACC AGC CAG TGT Leu Pro Glu Pro Ser Cys Pro Gln Leu Ala Thr Leu Thr Ser Gln Cys 835 840 845	2544
CTG ACC TAT GAG CCA ACC CAG AGG CCA TCA TTC CGC ACC ATC CTG CGT Leu Thr Tyr Glu Pro Thr Gln Arg Pro Ser Phe Arg Thr Ile Leu Arg 850 855 860	2592
GAC CTC ACC CGC GTG CAG CCC CAC AAT CTT GCT GAC GTC TTG ACT GTG Asp Leu Thr Arg Val Gln Pro His Asn Leu Ala Asp Val Leu Thr Val 865 870 875 880	2640
AAC CGG GAC TCA CCG GCC GTC GGA CCT ACT ACT TTC CAC AAG CGC TAT Asn Arg Asp Ser Pro Ala Val Gly Pro Thr Thr Phe His Lys Arg Tyr 885 890 895	2688
TTG AAA AAG ATC CGA GAT CTG GGC GAG GGT CAC TTC GGC AAG GTC AGC Leu Lys Lys Ile Arg Asp Leu Gly Glu Gly His Phe Gly Lys Val Ser 900 905 910	2736
TTG TAC TGC TAC GAT CCG ACC AAC GAC GGC ACT GGC GAG ATG GTG GCG Leu Tyr Cys Tyr Asp Pro Thr Asn Asp Gly Thr Gly Glu Met Val Ala 915 920 925	2784
GTG AAA GCC CTC AAG GCA GAC TGC GGC CCC CAG CAC CGC TCG GGC TGG Val Lys Ala Leu Lys Ala Asp Cys Gly Pro Gln His Arg Ser Gly Trp 930 935 940	2832
AAG CAG GAG ATT GAC ATT CTG CGC ACC CTC TAC CAC GAG CAC ATC ATC Lys Gln Glu Ile Asp Ile Leu Arg Thr Leu Tyr His Glu His Ile Ile 945 950 955 960	2880
AAG TAC AAG GGC TGC TGC GAG GAC CAA GGC GAG AAG TCG CTG CAG CTG Lys Tyr Lys Gly Cys Cys Glu Asp Gln Gly Glu Lys Ser Leu Gln Leu 965 970 975	2928
GTC ATG GAG TAC GTG CCC CTG GGC AGC CTC CGA GAC TAC CTG CCC CGG Val Met Glu Tyr Val Pro Leu Gly Ser Leu Arg Asp Tyr Leu Pro Arg 980 985 990	2976
CAC AGC ATC GGG CTG GCC CAG CTG CTG CTC TTC GCC CAG CAG ATC TGC His Ser Ile Gly Leu Ala Gln Leu Leu Leu Phe Ala Gln Gln Ile Cys 995 1000 1005	3024
GAG GGC ATG GCC TAT CTG CAC GCG CAC GAC TAC ATC CAC CGA GAC CTA Glu Gly Met Ala Tyr Leu His Ala His Asp Tyr Ile His Arg Asp Leu 1010 1015 1020	3072
GCC GCG CGC AAC GTG CTG CTG GAC AAC GAC AGG CTG GTC AAG ATC GGG Ala Ala Arg Asn Val Leu Leu Asp Asn Asp Arg Leu Val Lys Ile Gly	3120

1025	1030	1035	1040	
GAC TTT GGC CTA GCC AAG GCC GTG CCC GAA GGC CAC GAG TAC TAC CGC				3168
Asp Phe Gly Leu Ala Lys Ala Val Pro Glu Gly His Glu Tyr Tyr Arg	1045	1050	1055	
GTG CGC GAG GAT GGG GAC AGC CCC GTG TTC TGG TAT GCC CCA GAG TGC				3216
Val Arg Glu Asp Gly Asp Ser Pro Val Phe Trp Tyr Ala Pro Glu Cys	1060	1065	1070	
CTG AAG GAG TAT AAG TTC TAC TAT GCG TCA GAT GTC TGG TCC TTC GGG				3264
Leu Lys Glu Tyr Lys Phe Tyr Tyr Ala Ser Asp Val Trp Ser Phe Gly	1075	1080	1085	
GTG ACC CTG TAT GAG CTG CTG ACG CAC TGT GAC TCC AGC CAG AGC CCC				3312
Val Thr Leu Tyr Glu Leu Leu Thr His Cys Asp Ser Ser Gln Ser Pro	1090	1095	1100	
CCC ACG AAA TTC CTT GAG CTC ATA GGC ATT GCT CAG GGT CAG ATG ACA				3360
Pro Thr Lys Phe Leu Glu Leu Ile Gly Ile Ala Gln Gly Gln Met Thr	1105	1110	1115	1120
GTT CTG AGA CTC ACT GAG TTG CTG GAA CGA GGG GAG AGG CTG CCA CGG				3408
Val Leu Arg Leu Thr Glu Leu Leu Glu Arg Gly Glu Arg Leu Pro Arg	1125	1130	1135	
CCC GAC AAA TGT CCC TGT GAG GTC TAT CAT CTC ATG AAG AAC TGC TGG				3456
Pro Asp Lys Cys Pro Cys Glu Val Tyr His Leu Met Lys Asn Cys Trp	1140	1145	1150	
GAG ACA GAG GCG TCC TTT CGC CCA ACC TTC GAG AAC CTC ATA CCC ATT				3504
Glu Thr Glu Ala Ser Phe Arg Pro Thr Phe Glu Asn Leu Ile Pro Ile	1155	1160	1165	
CTG AAG ACA GTC CAT GAG AAG TAC CAA GGC CAG GCC CCT TCA GTG TTC				3552
Leu Lys Thr Val His Glu Lys Tyr Gln Gly Gln Ala Pro Ser Val Phe	1170	1175	1180	
AGC GTG TGC				3561
Ser Val Cys				
1185				

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1187 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Met	Pro	Leu	Arg	His	Trp	Gly	Met	Ala	Arg	Gly	Ser	Lys	Pro	Val	Gly
1				5					10					15	
Asp	Gly	Ala	Gln	Pro	Met	Ala	Ala	Met	Gly	Gly	Leu	Lys	Val	Leu	Leu
		20					25						30		
His	Trp	Ala	Gly	Pro	Gly	Gly	Gly	Glu	Pro	Trp	Val	Thr	Phe	Ser	Glu
	35					40						45			

Ser Ser Leu Thr Ala Glu Glu Val Cys Ile His Ile Ala His Lys Val
50 55 60

Gly Ile Thr Pro Pro Cys Phe Asn Leu Phe Ala Leu Phe Asp Ala Gln
65 70 75 80

Ala Gln Val Trp Leu Pro Pro Asn His Ile Leu Glu Ile Pro Arg Asp
85 90 95

Ala Ser Leu Met Leu Tyr Phe Arg Ile Arg Phe Tyr Phe Arg Asn Trp
100 105 110

His Gly Met Asn Pro Arg Glu Pro Ala Val Tyr Arg Cys Gly Pro Pro
115 120 125

Gly Thr Glu Ala Ser Ser Asp Gln Thr Ala Gln Gly Met Gln Leu Leu
130 135 140

Asp Pro Ala Ser Phe Glu Tyr Leu Phe Glu Gln Gly Lys His Glu Phe
145 150 155 160

Val Asn Asp Val Ala Ser Leu Trp Glu Leu Ser Thr Glu Glu Glu Ile
165 170 175

His His Phe Lys Asn Glu Ser Leu Gly Met Ala Phe Leu His Leu Cys
180 185 190

His Leu Ala Leu Arg His Gly Ile Pro Leu Glu Glu Val Ala Lys Lys
195 200 205

Thr Ser Phe Lys Asp Cys Ile Pro Arg Ser Phe Arg Arg His Ile Arg
210 215 220

Gln His Ser Ala Leu Thr Arg Leu Arg Leu Arg Asn Val Phe Arg Arg
225 230 235 240

Phe Leu Arg Asp Phe Gln Pro Gly Arg Leu Ser Gln Gln Met Val Met
245 250 255

Val Lys Tyr Leu Ala Thr Leu Glu Arg Leu Ala Pro Arg Phe Gly Thr
260 265 270

Glu Arg Val Pro Val Cys His Leu Arg Leu Leu Ala Gln Ala Glu Gly
275 280 285

Glu Pro Cys Tyr Ile Arg Asp Ser Gly Val Ala Pro Thr Asp Pro Gly
290 295 300

Pro Glu Ser Ala Ala Gly Pro Pro Thr His Glu Val Leu Val Thr Gly
305 310 315 320

Thr Gly Gly Ile Gln Trp Trp Pro Val Glu Glu Glu Val Asn Lys Glu
325 330 335

Glu Gly Ser Ser Gly Ser Ser Gly Arg Asn Pro Gln Ala Ser Leu Phe
340 345 350

Gly Lys Lys Ala Lys Ala His Lys Ala Phe Gly Gln Pro Ala Asp Arg
355 360 365

Pro Arg Glu Pro Leu Trp Ala Tyr Phe Cys Asp Phe Arg Asp Ile Thr

370	375	380
His Val Val Leu Lys Glu His Cys Val Ser Ile His Arg Gln Asp Asn 385 390 395 400		
Lys Cys Leu Glu Leu Ser Leu Pro Ser Arg Ala Ala Ala Leu Ser Phe 405 410 415		
Val Ser Leu Val Asp Gly Tyr Phe Arg Leu Thr Ala Asp Ser Ser His 420 425 430		
Tyr Leu Cys His Glu Val Ala Pro Pro Arg Leu Val Met Ser Ile Arg 435 440 445		
Asp Gly Ile His Gly Pro Leu Leu Glu Pro Phe Val Gln Ala Lys Leu 450 455 460		
Arg Pro Glu Asp Gly Leu Tyr Leu Ile His Trp Ser Thr Ser His Pro 465 470 475 480		
Tyr Arg Leu Ile Leu Thr Val Ala Gln Arg Ser Gln Ala Pro Asp Gly 485 490 495		
Met Gln Ser Leu Arg Leu Arg Lys Phe Pro Ile Glu Gln Gln Asp Gly 500 505 510		
Ala Phe Val Leu Glu Gly Trp Gly Arg Ser Phe Pro Ser Val Arg Glu 515 520 525		
Leu Gly Ala Ala Leu Gln Gly Cys Leu Leu Arg Ala Gly Asp Asp Cys 530 535 540		
Phe Ser Leu Arg Arg Cys Cys Leu Pro Gln Pro Gly Glu Thr Ser Asn 545 550 555 560		
Leu Ile Ile Met Arg Gly Ala Arg Ala Ser Pro Arg Thr Leu Asn Leu 565 570 575		
Ser Gln Leu Ser Phe His Arg Val Asp Gln Lys Glu Ile Thr Gln Leu 580 585 590		
Ser His Leu Gly Gln Gly Thr Arg Thr Asn Val Tyr Glu Gly Arg Leu 595 600 605		
Arg Val Glu Gly Ser Gly Asp Pro Glu Glu Gly Lys Met Asp Asp Glu 610 615 620		
Asp Pro Leu Val Pro Gly Arg Asp Arg Gly Gln Glu Leu Arg Val Val 625 630 635 640		
Leu Lys Val Leu Asp Pro Ser His His Asp Ile Ala Leu Ala Phe Tyr 645 650 655		
Glu Thr Ala Ser Leu Met Ser Gln Val Ser His Thr His Leu Ala Phe 660 665 670		
Val His Gly Val Cys Val Arg Gly Pro Glu Asn Ser Met Val Thr Glu 675 680 685		
Tyr Val Glu His Gly Pro Leu Asp Val Trp Leu Arg Arg Glu Arg Gly 690 695 700		

His	Val	Pro	Met	Ala	Trp	Lys	Met	Val	Val	Ala	Gln	Gln	Leu	Ala	Ser	705	710	715	720
Ala	Leu	Ser	Tyr	Leu	Glu	Asn	Lys	Asn	Leu	Val	His	Gly	Asn	Val	Cys	725	730	735	
Gly	Arg	Asn	Ile	Leu	Leu	Ala	Arg	Leu	Gly	Leu	Ala	Glu	Gly	Thr	Ser	740	745	750	
Pro	Phe	Ile	Lys	Leu	Ser	Asp	Pro	Gly	Val	Gly	Leu	Gly	Ala	Leu	Ser	755	760	765	
Arg	Glu	Glu	Arg	Val	Glu	Arg	Ile	Pro	Trp	Leu	Ala	Pro	Glu	Cys	Leu	770	775	780	
Pro	Gly	Gly	Ala	Asn	Ser	Leu	Ser	Thr	Ala	Met	Asp	Lys	Trp	Gly	Phe	785	790	795	800
Gly	Ala	Thr	Leu	Leu	Glu	Ile	Cys	Phe	Asp	Gly	Glu	Ala	Pro	Leu	Gln	805	810	815	
Ser	Arg	Ser	Pro	Ser	Glu	Lys	Glu	His	Phe	Tyr	Gln	Arg	Gln	His	Arg	820	825	830	
Leu	Pro	Glu	Pro	Ser	Cys	Pro	Gln	Leu	Ala	Thr	Leu	Thr	Ser	Gln	Cys	835	840	845	
Leu	Thr	Tyr	Glu	Pro	Thr	Gln	Arg	Pro	Ser	Phe	Arg	Thr	Ile	Leu	Arg	850	855	860	
Asp	Leu	Thr	Arg	Val	Gln	Pro	His	Asn	Leu	Ala	Asp	Val	Leu	Thr	Val	865	870	875	880
Asn	Arg	Asp	Ser	Pro	Ala	Val	Gly	Pro	Thr	Thr	Phe	His	Lys	Arg	Tyr	885	890	895	
Leu	Lys	Lys	Ile	Arg	Asp	Leu	Gly	Glu	Gly	His	Phe	Gly	Lys	Val	Ser	900	905	910	
Leu	Tyr	Cys	Tyr	Asp	Pro	Thr	Asn	Asp	Gly	Thr	Gly	Glu	Met	Val	Ala	915	920	925	
Val	Lys	Ala	Leu	Lys	Ala	Asp	Cys	Gly	Pro	Gln	His	Arg	Ser	Gly	Trp	930	935	940	
Lys	Gln	Glu	Ile	Asp	Ile	Leu	Arg	Thr	Leu	Tyr	His	Glu	His	Ile	Ile	945	950	955	960
Lys	Tyr	Lys	Gly	Cys	Cys	Glu	Asp	Gln	Gly	Glu	Lys	Ser	Leu	Gln	Leu	965	970	975	
Val	Met	Glu	Tyr	Val	Pro	Leu	Gly	Ser	Leu	Arg	Asp	Tyr	Leu	Pro	Arg	980	985	990	
His	Ser	Ile	Gly	Leu	Ala	Gln	Leu	Leu	Phe	Ala	Gln	Gln	Ile	Cys		995	1000	1005	
Glu	Gly	Met	Ala	Tyr	Leu	His	Ala	His	Asp	Tyr	Ile	His	Arg	Asp	Leu	1010	1015	1020	
Ala	Ala	Arg	Asn	Val	Leu	Leu	Asp	Asn	Asp	Arg	Leu	Val	Lys	Ile	Gly				

1025 1030 1035 1040
Asp Phe Gly Leu Ala Lys Ala Val Pro Glu Gly His Glu Tyr Tyr Arg
 1045 1050 1055
Val Arg Glu Asp Gly Asp Ser Pro Val Phe Trp Tyr Ala Pro Glu Cys
 1060 1065 1070
Leu Lys Glu Tyr Lys Phe Tyr Tyr Ala Ser Asp Val Trp Ser Phe Gly
 1075 1080 1085
Val Thr Leu Tyr Glu Leu Leu Thr His Cys Asp Ser Ser Gln Ser Pro
 1090 1095 1100
Pro Thr Lys Phe Leu Glu Leu Ile Gly Ile Ala Gln Gly Gln Met Thr
1105 1110 1115 1120
Val Leu Arg Leu Thr Glu Leu Leu Glu Arg Gly Glu Arg Leu Pro Arg
 1125 1130 1135
Pro Asp Lys Cys Pro Cys Glu Val Tyr His Leu Met Lys Asn Cys Trp
 1140 1145 1150
Glu Thr Glu Ala Ser Phe Arg Pro Thr Phe Glu Asn Leu Ile Pro Ile
 1155 1160 1165
Leu Lys Thr Val His Glu Lys Tyr Gln Gly Gln Ala Pro Ser Val Phe
1170 1175 1180
Ser Val Cys
1185

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1153 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Met Gln Tyr Leu Asn Ile Lys Glu Asp Cys Asn Ala Met Ala Phe Cys
1 5 10 15
Ala Lys Met Arg Ser Phe Lys Lys Thr Glu Val Lys Gln Val Val Pro
 20 25 30
Glu Pro Gly Val Glu Val Thr Phe Tyr Leu Ser Asp Arg Glu Pro Leu
 35 40 45
Arg Leu Gly Ser Gly Glu Tyr Thr Ala Glu Glu Leu Cys Ile Arg Ala
50 55 60
Ala Gln Glu Cys Ser Ile Ser Pro Leu Cys His Asn Leu Phe Ala Leu
65 70 75 80

Tyr	Asp	Glu	Ser	Thr	Lys	Leu	Trp	Tyr	Ala	Pro	Asn	Arg	Ile	Ile	Thr	
				85					90					95		
Val	Asp	Asp	Lys	Thr	Ser	Leu	Arg	Leu	His	Tyr	Arg	Met	Arg	Phe	Tyr	
			100					105					110			
Phe	Thr	Asn	Trp	His	Gly	Thr	Asn	Asp	Asn	Glu	Gln	Ser	Val	Trp	Arg	
		115					120					125				
His	Ser	Pro	Lys	Lys	Gln	Lys	Asn	Gly	Tyr	Glu	Lys	Lys	Arg	Val	Pro	
	130					135					140					
Glu	Ala	Thr	Pro	Leu	Leu	Asp	Ala	Ser	Ser	Leu	Glu	Tyr	Leu	Phe	Ala	
145					150					155					160	
Gln	Gly	Gln	Tyr	Asp	Leu	Ile	Lys	Phe	Leu	Ala	Pro	Ile	Arg	Asp	Pro	
				165					170					175		
Lys	Thr	Glu	Gln	Asp	Gly	His	Asp	Ile	Glu	Asn	Glu	Cys	Leu	Gly	Met	
			180					185					190			
Ala	Val	Leu	Ala	Ile	Ser	His	Tyr	Ala	Met	Met	Lys	Lys	Met	Gln	Leu	
		195					200					205				
Pro	Glu	Leu	Pro	Lys	Asp	Ile	Ser	Tyr	Lys	Arg	Tyr	Ile	Pro	Glu	Thr	
	210					215					220					
Leu	Asn	Lys	Ser	Ile	Arg	Gln	Arg	Asn	Leu	Leu	Thr	Arg	Met	Arg	Ile	
225					230					235					240	
Asn	Asn	Val	Phe	Lys	Asp	Phe	Leu	Lys	Glu	Phe	Asn	Asn	Lys	Thr	Ile	
			245						250					255		
Cys	Asp	Ser	Ser	Val	Ser	Thr	His	Asp	Leu	Lys	Val	Lys	Tyr	Leu	Ala	
			260					265					270			
Thr	Leu	Glu	Thr	Leu	Thr	Lys	His	Tyr	Gly	Ala	Glu	Ile	Phe	Glu	Thr	
		275					280					285				
Ser	Met	Leu	Leu	Ile	Ser	Ser	Glu	Asn	Glu	Leu	Ser	Arg	Cys	His	Ser	
	290					295					300					
Asn	Asp	Ser	Gly	Asn	Val	Leu	Tyr	Glu	Val	Met	Val	Thr	Gly	Asn	Leu	
305					310					315					320	
Gly	Ile	Gln	Trp	Arg	Gln	Lys	Pro	Asn	Val	Val	Pro	Val	Glu	Lys	Glu	
				325					330					335		
Lys	Asn	Lys	Leu	Lys	Arg	Lys	Lys	Leu	Glu	Tyr	Asn	Lys	His	Lys	Lys	
			340					345					350			
Asp	Asp	Glu	Arg	Asn	Lys	Leu	Arg	Glu	Glu	Trp	Asn	Asn	Phe	Ser	Tyr	
		355					360					365				
Phe	Pro	Glu	Ile	Thr	His	Ile	Val	Ile	Lys	Glu	Ser	Val	Val	Ser	Ile	
	370					375					380					
Asn	Lys	Gln	Asp	Asn	Lys	Asn	Met	Glu	Leu	Lys	Leu	Ser	Ser	Arg	Glu	
385					390					395					400	
Glu	Ala	Leu	Ser	Phe	Val	Ser	Leu	Val	Asp	Gly	Tyr	Phe	Arg	Leu	Thr	
				405					410					415		

Ala Asp Ala His His Tyr Leu Cys Thr Asp Val Ala Pro Pro Leu Ile
420 425 430

Val His Asn Ile Gln Asn Gly Cys His Gly Pro Ile Cys Thr Glu Tyr
435 440 445

Ala Ile Asn Lys Leu Arg Gln Glu Gly Ser Glu Glu Gly Met Tyr Val
450 455 460

Leu Arg Trp Ser Cys Thr Asp Phe Asp Asn Ile Leu Met Thr Val Thr
465 470 475 480

Cys Phe Glu Lys Ser Glu Val Leu Gly Gly Gln Lys Gln Phe Lys Asn
485 490 495

Phe Gln Ile Glu Val Gln Lys Gly Arg Tyr Ser Leu His Gly Ser Met
500 505 510

Asp His Phe Pro Ser Leu Arg Asp Leu Met Asn His Leu Lys Lys Gln
515 520 525

Ile Leu Arg Thr Asp Asn Ile Ser Phe Val Leu Lys Arg Cys Cys Gln
530 535 540

Pro Lys Pro Arg Glu Ile Ser Asn Leu Leu Val Ala Thr Lys Lys Ala
545 550 555 560

Gln Glu Trp Gln Pro Val Tyr Ser Met Ser Gln Leu Ser Phe Asp Arg
565 570 575

Ile Leu Lys Lys Asp Ile Ile Gln Gly Glu His Leu Gly Arg Gly Thr
580 585 590

Arg Thr His Ile Tyr Ser Gly Thr Leu Leu Asp Tyr Lys Asp Glu Glu
595 600 605

Gly Ile Ala Glu Glu Lys Lys Ile Lys Val Ile Leu Lys Val Leu Asp
610 615 620

Pro Ser His Arg Asp Ile Ser Leu Ala Phe Phe Glu Ala Ala Ser Met
625 630 635 640

Met Arg Gln Val Ser His Lys His Ile Val Tyr Leu Tyr Gly Val Cys
645 650 655

Val Arg Asp Val Glu Asn Ile Met Val Glu Glu Phe Val Glu Gly Gly
660 665 670

Pro Leu Asp Leu Phe Met His Arg Lys Ser Asp Ala Leu Thr Thr Pro
675 680 685

Trp Lys Phe Lys Val Ala Lys Gln Leu Ala Ser Ala Leu Ser Tyr Leu
690 695 700

Glu Asp Lys Asp Leu Val His Gly Asn Val Cys Thr Lys Asn Leu Leu
705 710 715 720

Leu Ala Arg Glu Gly Ile Asp Ser Asp Ile Gly Pro Phe Ile Lys Leu
725 730 735

Ser Asp Pro Gly Ile Pro Val Ser Val Leu Thr Arg Gln Glu Cys Ile
740 745 750

Glu Arg Ile Pro Trp Ile Ala Pro Glu Cys Val Glu Asp Ser Lys Asn
 755 760 765
 Leu Ser Val Ala Ala Asp Lys Trp Ser Phe Gly Thr Thr Leu Trp Glu
 770 775 780
 Ile Cys Tyr Asn Gly Glu Ile Pro Leu Lys Asp Lys Thr Leu Ile Glu
 785 790 795 800
 Lys Glu Arg Phe Tyr Glu Ser Arg Cys Arg Pro Val Thr Pro Ser Cys
 805 810 815
 Lys Glu Leu Ala Asp Leu Met Thr Arg Cys Met Asn Tyr Asp Pro Asn
 820 825 830
 Gln Arg Pro Phe Phe Arg Ala Ile Met Arg Asp Ile Asn Lys Leu Glu
 835 840 845
 Glu Gln Asn Pro Asp Ile Val Ser Glu Lys Gln Pro Thr Thr Glu Val
 850 855 860
 Asp Pro Thr His Phe Glu Lys Arg Phe Leu Lys Arg Ile Arg Asp Leu
 865 870 875 880
 Gly Glu Gly His Phe Gly Lys Val Glu Leu Cys Arg Tyr Asp Pro Glu
 885 890 895
 Gly Asp Asn Thr Gly Glu Gln Val Ala Val Lys Ser Leu Lys Pro Glu
 900 905 910
 Ser Gly Gly Asn His Ile Ala Asp Leu Lys Lys Glu Ile Glu Ile Leu
 915 920 925
 Arg Asn Leu Tyr His Glu Asn Ile Val Lys Tyr Lys Gly Ile Cys Met
 930 935 940
 Glu Asp Gly Gly Asn Gly Ile Lys Leu Ile Met Glu Phe Leu Pro Ser
 945 950 955 960
 Gly Ser Leu Lys Glu Tyr Leu Pro Lys Asn Lys Asn Lys Ile Asn Leu
 965 970 975
 Lys Gln Gln Leu Lys Tyr Ala Ile Gln Ile Cys Lys Gly Met Asp Tyr
 980 985 990
 Leu Gly Ser Arg Gln Tyr Val His Arg Asp Leu Ala Ala Arg Asn Val
 995 1000 1005
 Leu Val Glu Ser Glu His Gln Val Lys Ile Gly Asp Phe Gly Leu Thr
 1010 1015 1020
 Lys Ala Ile Glu Thr Asp Lys Glu Tyr Tyr Thr Val Lys Asp Asp Arg
 1025 1030 1035 1040
 Asp Ser Pro Val Phe Trp Tyr Ala Pro Glu Cys Leu Ile Gln Cys Lys
 1045 1050 1055
 Phe Tyr Ile Ala Ser Asp Val Trp Ser Phe Gly Val Thr Leu His Glu
 1060 1065 1070
 Leu Leu Thr Tyr Cys Asp Ser Asp Ser Phe Pro Met Ala Leu Phe Leu
 1075 1080 1085

Lys Met Ile Gly Pro Thr His Gly Gln Met Thr Val Thr Arg Leu Val
1090 1095 1100

Asn Thr Leu Lys Glu Gly Lys Arg Leu Pro Cys Pro Pro Asn Cys Pro
1105 1110 1115 1120

Asp Glu Val Tyr Gln Leu Met Arg Lys Cys Trp Glu Phe Gln Pro Ser
1125 1130 1135

Asn Arg Thr Thr Phe Gln Asn Leu Ile Glu Gly Phe Glu Ala Leu Leu
1140 1145 1150

Lys

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 17 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Ala Lys Leu Leu Pro Leu Asp Lys Asp Tyr Tyr Val Val Arg Glu Pro
1 5 10 15

Gly

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1099 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: not relevant
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Met Ala Pro Pro Ser Glu Glu Thr Pro Leu Ile Pro Gln Arg Ser Cys
1 5 10 15

Ser Leu Ser Ser Ser Glu Ala Gly Ala Leu His Val Leu Leu Pro Pro
20 25 30

Arg Gly Pro Gly Pro Pro Gln Arg Leu Ser Phe Ser Phe Gly Asp Tyr
35 40 45

Leu Ala Glu Asp Leu Cys Val Arg Ala Ala Lys Ala Cys Gly Ile Leu
50 55 60

Pro Val Tyr His Ser Leu Phe Ala Leu Ala Thr Glu Asp Phe Ser Cys
65 70 75 80

Trp Phe Pro Pro Ser His Ile Phe Cys Ile Glu Asp Val Asp Thr Gln

85	90	95
Val Leu Val Tyr Arg Leu Arg Phe Tyr Phe Pro Asp Trp Phe Gly Leu	100	105 110
Glu Thr Cys His Arg Phe Gly Leu Arg Lys Asp Leu Thr Ser Ala Ile	115	120 125
Leu Asp Leu His Val Leu Glu His Leu Phe Ala Gln His Arg Ser Asp	130	135 140
Leu Val Ser Gly Arg Leu Pro Val Gly Leu Ser Met Lys Glu Gln Gly	145	150 155 160
Glu Phe Leu Ser Leu Ala Val Leu Asp Leu Ala Gln Met Ala Arg Glu	165	170 175
Gln Ala Gln Arg Pro Gly Glu Leu Leu Lys Thr Val Ser Tyr Lys Ala	180	185 190
Cys Leu Pro Pro Ser Leu Arg Asp Val Ile Gln Gly Gln Asn Phe Val	195	200 205
Thr Arg Arg Arg Ile Arg Arg Thr Val Val Leu Ala Leu Leu Pro Cys	210	215 220
Gly Arg Leu Pro Gly Arg Pro Tyr Ala Leu Met Ala Lys Tyr Ile Leu	225	230 235 240
Asp Leu Glu Arg Leu His Pro Ala Ala Thr Thr Glu Thr Phe Arg Val	245	250 255
Gly Leu Pro Gly Ala Gln Glu Glu Pro Gly Leu Leu Arg Val Ala Gly	260	265 270
Asp Asn Gly Ile Pro Trp Ser Ser Asn Asp Glu Leu Phe Gln Thr Phe	275	280 285
Cys Asp Phe Pro Glu Ile Val Asp Val Ser Ile Asn Gln Ala Pro Arg	290	295 300
Val Gly Pro Ala Gly Glu His Arg Leu Val Thr Val Thr Arg Met Asp	305	310 315 320
Gly His Ile Leu Glu Ala Glu Phe Pro Gly Leu Pro Glu Ala Leu Ser	325	330 335
Phe Val Ala Leu Val Asp Gly Tyr Phe Arg Leu Ile Cys Asp Ser Arg	340	345 350
His Tyr Phe Cys Lys Glu Val Ala Pro Pro Arg Leu Leu Glu Glu Glu	355	360 365
Ala Asp Val Cys His Gly Pro Ile Thr Leu Asp Phe Ala Ile His Lys	370	375 380
Leu Lys Ala Ala Gly Ser Leu Pro Gly Thr Tyr Ile Leu Arg Arg Ser	385	390 395 400
Pro Gln Asp Tyr Asp Ser Phe Leu Leu Thr Ala Cys Val Gln Thr Pro	405	410 415

Leu Gly Pro Asp Tyr Lys Gly Cys Leu Ile Arg Gln Asp Pro Ser Gly
 420 425 430
 Ala Phe Ser Leu Val Gly Leu Ser Gln Pro His Arg Ser Leu Arg Glu
 435 440 445
 Leu Leu Ala Ala Cys Trp Asn Ser Gly Leu Arg Val Asp Gly Ala Ala
 450 455 460
 Leu Tyr Leu Thr Ser Cys Cys Ala Pro Arg Pro Lys Glu Lys Ser Asn
 465 470 475 480
 Leu Ile Val Val Arg Arg Gly Cys Asn Pro Ala Pro Ala Pro Gly Cys
 485 490 495
 Ser Pro Ser Cys Cys Ala Leu Thr Gln Leu Ser Phe His Thr Ile Pro
 500 505 510
 Thr Asp Ser Leu Glu Trp His Glu Asn Leu Gly His Gly Ser Phe Thr
 515 520 525
 Lys Ile Phe Arg Gly Ser Arg Arg Glu Val Val Asp Gly Glu Thr His
 530 535 540
 Asp Ser Glu Val Leu Leu Lys Val Met Asp Ser Arg His Arg Asn Cys
 545 550 555 560
 Met Glu Ser Phe Leu Glu Ala Ala Ser Leu Met Ser Gln Val Ser Tyr
 565 570 575
 Pro His Leu Val Leu Leu His Gly Val Cys Met Ala Gly Asp Ser Ile
 580 585 590
 Met Val Gln Glu Phe Val Tyr Leu Gly Ala Ile Asp Met Tyr Leu Arg
 595 600 605
 Lys Arg Gly His Leu Val Ser Ala Ser Trp Lys Leu Gln Val Thr Lys
 610 615 620
 Gln Leu Ala Tyr Ala Leu Asn Tyr Leu Glu Asp Lys Gly Leu Pro His
 625 630 635 640
 Gly Asn Val Ser Ala Arg Lys Val Leu Leu Ala Arg Glu Gly Gly Asp
 645 650 655
 Gly Asn Pro Pro Phe Ile Lys Leu Ser Asp Pro Gly Val Ser Pro Thr
 660 665 670
 Val Leu Ser Leu Glu Met Leu Thr Asp Arg Ile Pro Trp Val Ala Pro
 675 680 685
 Glu Cys Leu Gln Glu Ala Gln Thr Leu Cys Leu Glu Ala Asp Lys Trp
 690 695 700
 Gly Phe Gly Ala Thr Thr Trp Glu Val Phe Gln Arg Gly Pro Ala His
 705 710 715 720
 Ile Thr Ser Leu Glu Pro Ala Lys Lys Leu Lys Phe Tyr Glu Asp Gln
 725 730 735
 Gly Gln Leu Pro Ala Leu Lys Trp Thr Glu Leu Ala Gly Leu Ile Thr
 740 745 750

Gln Cys Met Ala Tyr Asp Pro Gly Arg Arg Pro Ser Phe Arg Ala Ile
755 760 765

Leu Arg Asp Leu Asn Gly Leu Ile Thr Ser Asp Tyr Glu Leu Leu Ser
770 775 780

Asp Pro Thr Pro Gly Ile Pro Ser Pro Arg Asp Glu Leu Cys Val Ala
785 790 795 800

Gly Ala Gln Leu Tyr Ala Cys Gln Asp Pro Ala Ile Phe Glu Glu Arg
805 810 815

His Leu Lys Tyr Ile Ser Leu Leu Gly Lys Gly Asn Phe Gly Ser Val
820 825 830

Glu Leu Cys Arg Tyr Asp Pro Leu Gly Asp Asn Thr Gly Pro Leu Val
835 840 845

Ala Val Lys Gln Leu Gln His Ser Val Pro Asp Gln Gln Arg Asp Phe
850 855 860

Gln Arg Glu Ile Gln Ile Leu Lys Ala Leu His Ser Asp Phe Ile Val
865 870 875 880

Lys Tyr Arg Gly Val Ser Tyr Gly Pro Gly Arg Gln Ser Leu Arg Leu
885 890 895

Val Met Glu Tyr Leu Pro Ser Gly Cys Leu Arg Asp Leu Leu Gln Arg
900 905 910

His Arg Gly Leu His Thr Asp Arg Leu Leu Leu Phe Ala Trp Gln Ile
915 920 925

Cys Lys Gly Met Glu Tyr Leu Gly Ala Arg Arg Cys Val His Arg Asp
930 935 940

Leu Ala Ala Arg Asn Ile Leu Val Glu Ser Glu Ala His Val Lys Ile
945 950 955 960

Ala Asp Phe Gly Leu Ala Lys Leu Leu Pro Leu Gly Lys Asp Tyr Tyr
965 970 975

Val Val Arg Glu Pro Gly Gln Ser Pro Ile Phe Trp Tyr Ala Pro Glu
980 985 990

Ser Leu Ser Asp Asn Ile Phe Ser Arg Gln Ser Asp Val Trp Ser Phe
995 1000 1005

Gly Val Val Leu Tyr Glu Leu Phe Thr Tyr Cys Asp Lys Ser Cys Ser
1010 1015 1020

Pro Ser Ala Glu Phe Leu Arg Met Met Gly Pro Glu Arg Glu Gly Pro
1025 1030 1035 1040

Pro Leu Cys Arg Leu Leu Glu Leu Leu Ala Glu Gly Arg Arg Leu Pro
1045 1050 1055

Pro Pro Pro Thr Cys Pro Thr Glu Val Gln Glu Leu Met Gln Leu Cys
1060 1065 1070

Trp Ala Pro Glu Pro His Asp Arg Pro Ala Phe Ala Thr Leu Ser Pro
1075 1080 1085

Gln Leu Asp Pro Leu Trp Arg Gly Arg Pro Gly
1090 1095

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Lys Asp Tyr Tyr
1